



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 176764**

**TO: Walter Schlapkohl**  
**Location: rem/2b79/2c70**  
**Art Unit: 1636**  
**Tuesday, January 17, 2006**  
**Case Serial Number: 09/671687**

**From: Barb O'Bryen**  
**Location: Biotech-Chem Library**  
**Remsen 1a69**  
**Phone: 571-272-2518**

*BOB*  
**barbara.obryen@uspto.gov**

### **Search Notes**



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[Text Entry](#) | [EmblEntry](#)

**Go to:** [General](#) [Description](#) [References](#) [Cross-references](#) [Sequence](#)

### General Information

Primary Accession # AJ250014  
Accession # AJ250014  
Entry Name EMBL:HSA250014  
Molecule Type mRNA  
Sequence Length 5371  
Entry Division HUM  
Sequence Version AJ250014.1  
Creation Date 03-JUN-2000  
Modification Date 16-JUN-2000

### Description

Description Homo sapiens mRNA for Familial Cyldromatosis cyld gene  
Keywords cyld gene; Familial Cyldromatosis.;  
Organism Homo sapiens (human)  
Organism Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheri  
Classification Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

### References

1. Stratton,M.R.; Submitted (29-NOV-1999) to the EMBL/GenBank/DDBJ databases. Stratton M.R., Cancer Genetics, Institute of Cancer Research, 15 Cotswold Rd, Sutton,, Surrey. S15 2NG., UNITED KINGDOM.  
Position 1-5371
2. Bignell,G.R.; Brown,C.; Biggs,P.J.; Lakhani,S.R.; Jones,C.; Hansen,J.; Blair,E.; Hofman Siebert,R.; Turner,G.; Evans,D.G.; Schrander-Stumpel,C.; Beemer,F.A.; Van Den Ouwe Halley,D.; Delpech,B.; Cleveland,M.G.; Leigh,I.; Leisti,J.; Rasmussen,S.; Wallace,M.R.; Fenske,C.; Banerjee,P.; Oiso,N.; Chaggar,R.; Merrett,S.; Leonard,N.; Huber,M.; Hohl,D; Chapman,P.; Burn,J.; Swift,S.; Smith,A.; Ashworth,A.; Stratton,M.R.;  
**Identification of the familial cyldromatosis tumor suppressor gene.**  
Nat. Genet. 25(2):160-165 (2000)  
DOI [10.1038/76006](#)  
Pubmed [10835629](#)

### Database Cross-references

**GDB** [701216](#).

**Features**

Key	Location	Qualifier	Value
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		<b>mol_type</b>	mRNA
		<b>organism</b>	Homo sapiens
		<b>map</b>	16q12 - q13
<b><u>cds</u></b>	392..3262	<b>db_xref</b>	<a href="#">GOA:Q9NQC7</a>
		<b>db_xref</b>	<a href="#">InterPro:IPR000938</a>
		<b>db_xref</b>	<a href="#">InterPro:IPR001394</a>
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		<b>db_xref</b>	<a href="#">PDB:1WHL</a>
		<b>db_xref</b>	<a href="#">PDB:1WHM</a>
		<b>db_xref</b>	<a href="#">UniProtKB/Swiss-Prot:Q9NQC7</a>
		<b>note</b>	Familial Cylindromatosis Gene
		<b>gene</b>	cyld
		<b>function</b>	tumour suppressor/recessive oncogene
		<b>experiment</b>	experimental evidence, no additional details reco
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		<b>translation</b>	<div><div>&gt;CAB93533</div><div>MSSGLWSQEKVTSPYWEERIFYLLLLQECSVTDKQTQK</div><div>PSAKGKKNQIGLKILEQPHAVLFVDEKDVVEINEKFT</div><div>KGLQIDVGCPVKVQLRSGEKFPGVVFRGPLLAERT</div><div>YQ GKQLFQCDEDCGVFVALDKLELIEDDDTALES DYA</div><div>◀</div></div>

**Sequence**

Characteristics	<b>Length:</b> 5371 BP, <b>A Count:</b> 1600, <b>C Count:</b> 950, <b>G Count:</b> 1183, <b>T Count:</b> 1638, <b>Other:</b> Count:0
Sequence	

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 15, 2006, 23:03:04 ; Search time 9744 Seconds  
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5385.028 Million cell updates/sec

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Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 33

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 90%

Maximum Match 100%

Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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5	4983	99.0	4664	32	Sequence 1729, Ap
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7	4983	99.0	4668	23	Sequence 4309, Ap

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9	4983	99.0	4668	23	US-09-397-424-5019	Sequence 5019, Ap
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12	4983	99.0	4668	24	US-09-432-737-1278	Sequence 1278, Ap
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32	4601	91.4	2845	28	US-09-629-469A-18842	Sequence 18842, A
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ALIGNMENTS

RESULT 1

US-09-671-687a-2

Sequence 2, Application US/09671687A

GENERAL INFORMATION:

APPLICANT: WALLACH, David

APPLICANT: KOVALENKO, Andrei

APPLICANT: CANTARELLA, Giuseppe

TITLE OF INVENTION: INHIBITOR OF NF-kB ACTIVATOR

FILE REFERENCE: WALLACH-25

CURRENT APPLICATION NUMBER: US/09/671,687A

CURRENT FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: 09/646,403

PRIOR FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: IL 126024

PRIOR FILING DATE: 1998-09-01

PRIOR APPLICATION NUMBER: IL 134604

PRIOR FILING DATE: 2000-02-17

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 3715

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: (18)..(18)

OTHER INFORMATION: n is either a, c, g, or t.

NAME/KEY: misc feature

LOCATION: (22)..(22)

OTHER INFORMATION: n is either a, c, g, or t.

NAME/KEY: misc feature

LOCATION: (756)..(756)

OTHER INFORMATION: n is either a, c, g, or t.

NAME/KEY: misc feature

LOCATION: (1348)..(1348)

OTHER INFORMATION: n is either a, c, g, or t.

US-09-671-687a-2

Alignment Scores:

Pred. No.: 0

Score: 4992.00

Percent Similarity: 99.58%

Best Local Similarity: 99.58%

Length: 3715

Matches: 949

Conservative: 0

Mismatches: 0

Query Match:	99.17%	Indels:	4
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Qy	81	ValLeuPheValAspGlu---AspValValGluLeuLeuGlnLysPheThrGluLeuLeu	99
Db	737	GTTCTCTTGTGATGAAANGGATGTTGTAGAGATAAATGAAAAAGTTTACAGAGTTACTT	796
Qy	100	LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer	119
Db	797	TTGGCAATTACCAATTGTGAGGAGAGGTTTCTGCTGTTTAAAAACAGAAAACAGATAAGT	856
Qy	120	LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu	139
Db	857	AAAGGCTTCCAAATAGAGCTGGGCTGCTCTGTGAAGTACAGCTGAGATCTGGGGAAGAA	916
Qy	140	LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly	159
Db	917	AAATTTCTGGAGTTGTACGCTTACAGAGGACCCCTGTTTAGCAGAGAGACAGTCTCCGGA	976
Qy	160	IlePhePheGlyValGluLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal	179
Db	977	ATATTTCTGGAGTTGAAATTGCTGGAAGAGGTCGTGTCGTCGTCGTCGTCGTCGTCGTCG	1036
Qy	180	TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp	198
Db	1037	TACCAAGGAAACAGCTTTTTCAGTGTGATGAAGATTTGTCGCTGTTTGTTCATTTGAC	1096
Qy	199	LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly	218
Db	1097	AAGCTAGAACTCATAGAAGATGATGACACATGCAATTTGGAAGATGATTACGAGGTCCTGGG	1156
Qy	219	AspThrMetGlnValGluLeuProPheGlnLeuLeuSerArgValSerLeuLysGly	238
Db	1157	GACAAATGCAAGGTCGAACTTCTCTTTCGAAATAAACTCCAGAGTTTCTTTGAAGGTT	1216
Qy	239	GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer	258
Db	1217	GGAGAAACAATAGAACTTGGAAACAGTTATATTTCTGTGATGTTTTCAGGAGAAAGAAC	1276
Qy	259	LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe	278
Db	1277	TTAGGATATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1336
Qy	279	AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleLeu	297
Db	1337	GATGGAGTCANCTTTTGTAGTTTTTGTGCGTGTGTTGAAAGTACAAATTTCTATTGCA	1396
Qy	298	AspIleIleProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSer	317
Db	1397	GATATCATCCAGAGTGTGACGAGAAAGGAGGCTTCCCAAACTTGTCTTTTATGTCAT	1456
Qy	318	ArgGlyValGlyAspLysGlySerSerSerHisAsnLysProLysAlaThrGlySerThr	337
Db	1457	AGAGTGTGGGACAAAGGTTTCATCCAGTCATATAAACCAAGGCTTACAGGATCTACC	1516

```
QY 338 SerAspProGlyAenArg---ArgSerGluLeuPheTyrThrLeuAenGlySerSerVal 356
Db 1517 TCAGACCCCTGGAATAAGAACAGACTGGAATATATTTATACCTTAAATGGGTCTTCTGTT 1576
QY 357 AspSerGlnProGlnSerLysSerLysAsnThrTptfyrIleAspGluValAlaGluAsp 376
Db 1577 GACTCAACACCAATCCAAATCAAAAATACATGGTACATTGATGATGAAGTTGCAGAGAC 1636
QY 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln 396
Db 1637 CCTGCAAAATCTCTTACAGAGATATCTACAGACTTTTGACCGTTCTTCAACCACTCCAG 1696
QY 397 ProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416
Db 1697 CCTCCCTCTGTGAACCTCACTGACCACCGAGAACAAGATTCCACTCTTTTACCATTTCAGTCTC 1756
QY 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436
Db 1757 ACCAAGATGCCAATACCAATGGAAGTATTGGCCACAGTCCACTTCTCTGTACGCCAG 1816
QY 437 SerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro 456
Db 1817 TCTGTAATGGAAGAGCTAAACACTGCACCCGTCACAGAGAGTCCACCTTGGCCATGCT 1876
QY 457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476
Db 1877 CCTGGGAACCTCACATGCTGTAGAAGTGGGCTCATTTGGCTGAAGTTAAGGAGAAACCTCT 1936
QY 477 PheTyrGlyValIleArgTptIleGlyGlnProGlyLeuAsnGluValLeuAlaGly 496
Db 1937 TTTCTATGGGGTAATCCGTTGGATCGGTACGCCACCAAGAGTGAATGAAGTGCCTGGTGA 1996
QY 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516
Db 1997 CTGGAACCTGGAAGATGAGTGTGAGGCTGTACGATGGAACCTTCAGAGGCATCTGGTAT 2056
QY 517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSer 536
Db 2057 TTCACCTGTGCCCTGGAAGAGGCGCTGTTGTGAACCTGAAGAGCTGCAGCCCTGACTCT 2116
QY 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556
Db 2117 AGGTGTTGCATCATTTGACGCGGTTTCCAATCAGATTGAGCGCTGTAACTCTTTAGCATTT 2176
QY 557 GlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGly 576
Db 2177 GGAGGCTACTTAAGTGAAGTAGTAGAAGAAAATACTCCACAAAATGGAAAAGAGGC 2236
QY 577 LeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596
Db 2237 TTGGAGATATGATTGGGAAGAGAAGAGGATCCAGGTCATTACAAATCTTGTACTTTA 2296
QY 597 AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg 616
Db 2297 GACTCAACCTATTCTGCTATTATTGCTTTTGTGTTCTGTTCTGACACTGTGTTACTTGA 2356
QY 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuArgThrGlu 636
Db 2357 CCCAAAGAAAAGAACGATGTAGAATATTATAGTGAACCCCAAGAGCTACTGAGACAGAA 2416
QY 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656
Db 2417 ATTGTTAACTCTGAGAATATATGATATGTGTGGCCACAAAATTTATGAACCTGAGG 2476
QY 657 LysIleLeuGluLysValGluAlaAlaSerGlyPheThrSerGluGluLysAspProGlu 676
Db 2477 AAAATACTTGAAGGTGGAGGCTGCATCAGGATTTACCTCTCAAGAAAAGATCTCTGAG 2536
QY 677 GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArg 696
Db 2537 GAATCTTGAATATTCTGTTTCATCATATTTTAAAGGTGAACCTTTGCTTAAAAATAAGA 2596
QY 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716
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Db 2597 TCAGACGTCAAAAGGTACAAGATTGTTACTTCTATCAAAATTTTATGGAAAAAATGAG 2656
QY 717 LysValGlyValProThrIleGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeu 736
Db 2657 AAAGTTGGCGCTGCCACAAATTCAGCAGTTGTAGATGGTCTTTTATCAACAGTAACTG 2716
QY 737 LysPheAlaGluAlaProSerCysLeuIleLeuGlnMetProArgPheGlyLysAspPhe 756
Db 2717 AAATTTGAGAGGCACCATCATGTCGATTATTCAGATGCCTCGATTTTGGAAAGACTTT 2776
QY 757 LysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuLys 776
Db 2777 AAACATATTAAAAAATTTTCTCTCTCGAATATAATAACAGATTTTACTTGAAGAC 2836
QY 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr 796
Db 2837 ACTCCACAGACAGTCCCGGATATGTGGAGGGCTTGCAATGTATGAGTAGAGAATGCTAC 2896
QY 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln 816
Db 2897 GACGATCCGACATCTCAGCTGGAAAAATCAAGCAGTTTGTAAAAACCTGCAACACTCAA 2956
QY 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836
Db 2957 GTCCACCTTCAATCCGAAGAGGCTGAATCATATAATATAACCCAGTGTCACTTCCCAAGAC 3016
QY 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856
Db 3017 TTACCCGACTGGGACTGGAGACACGGCTGCATCCCTTGCCAGAAATATGGAGTTATTGCT 3076
QY 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876
Db 3077 GTTCTGTGATAGAAACAAGCCACTATGTGCTTTTGTGAAGTATGGAGAGGACGATTCT 3136
QY 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896
Db 3137 GCCTGGCTCTCTTTGACAGCATGGCCGATCGGATGCTGCTCAGATGCTTCAACATT 3196
QY 897 ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu 916
Db 3197 CCTCAAGTCAACCCATGCCAGAGTAGGAGAGTACTTGAAGATGTCTCTCGAAGACCTG 3256
QY 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936
Db 3257 CATTCCTTGACCTCCAGAGAAATCCAAGGCTGTCCAGAGACTGCTTTGTGATGCATAT 3316
QY 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3317 ATGTCATGTACCAGAGTCCCAACATGAGTTGTACAAA 3355

RESULT 2
US-09-522-303-1293
; Sequence 1293, Application US/09522303
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; TITLE OF INVENTION: HUMAN MAMMARY EPITHELIAL LIBRARY
; FILE REFERENCE: 1600.1086-001
; CURRENT APPLICATION NUMBER: US/09/522,303
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 60/123,393
; EARLIER FILING DATE: 1999-03-08
; NUMBER OF SEQ ID NOS: 1353
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 1293
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(4661)
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OTHER INFORMATION: n = A, T, C or G  
US-09-522-303-1293

## Alignment Scores:

Pred. No.:	0	Length:	4661
Score:	4983.00	Matches:	948
Percent Similarity:	99.48%	Conservative:	0
Best Local Similarity:	99.48%	Mismatches:	1
Query Match:	98.99%	Indels:	4
DB:	25	Gaps:	4

US-09-671-687A-3 (1-949) x US-09-522-303-1293 (1-4661)

Qy	1	MetSerSerGlyLeuTTPSerGlnGluLysValThrSerProTyrTrpGluGluArgile	20
Db	231	ATGAGTTACGGCTTATGGAGCAAGAAAAGTCACTTCCCTACTGGGAAGACGGATT	290
Qy	21	PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys	40
Db	291	TTTTACTTGTCTTCAAGAATGAGCTTACAGACAAACACAAAAGCTCCTTAAA	350
Qy	41	ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgile	60
Db	351	GTACCGAAGGAGATATAGGACAGTATATCAAGATCGTTCTGTGGGCGCATTC	410
Qy	61	ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnGlnProHisAla	80
Db	411	CCTTCTCAAAAGGCAAGAAAATCAGATTGGATTAAATAATCTAGAGCAACCT	470
Qy	81	ValLeuPheValAspGlu---AspValValIleLeuLeuLysPheThrGluLeuLeu	99
Db	471	GTTCTCTTTGTTGATGAAAAGGATGTTGTAGAGATAAATGAAAGTTTCA	530
Qy	100	LeuAlaIleThrAsnCysGluGluAurPheSerLeuPheLysAsnArgLeuSer	119
Db	531	TTGGCAATTACCAATTGTGAGGAGAGGTCAGCCCTGTTTAAAAACAGAA	590
Qy	120	LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGlu	139
Db	591	AAAGGCTCCAAATAGACGCTGGGCTGCTGTGTGAAGTACAGCTGAGAT	650
Qy	140	LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSer	159
Db	651	AAATTTCTGGAGTTGTACGCTTCAGAGGACCCCTGTTAGCAGAGAGAC	710
Qy	160	IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGly	179
Db	711	ATATTTCTTGGAGTTGAATTGCTGGAAGAGGTCGTGTCAAGGTTTCACT	770
Qy	180	TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeu	198
Db	771	TACCAAGGGAACACAGCTTTTTCAGTGTGATGAGATTTGTGGCGTGTGTT	830
Qy	199	LysLeuLeuLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly	218
Db	831	AAGCTAGAACTCATAGAGATGATGACATGTCATTGGAAAGTGAATACG	278
Qy	219	AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly	238
Db	891	GACACAATGAGGTCGAACTTCTCTTCTTGGAAATAACTCCAGATTTCTT	290
Qy	239	GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer	258
Db	951	GGAGAAACAATAGAACTCGGAACAGTTATATTTCTGTGATGTTTTC	310
Qy	259	LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTyrAspGlyArgPhe	278
Db	1011	TTAGGATATTTTGTGTGTGTGGAATGGATTAACCTTATTTGGCACTGG	330
Qy	279	AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn	297
Db	1071	GATGGAGTGCAGCTTTGTAGTTTTCGGTGTGTGTGAAGTCAATTTCTAT	350

Qy	298	AspIleIleProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSer	317
Db	1131	GATATCATCCAGAGAGTGTGACGAGAAAGGAGGCTCCCAACTTGGCTTTATG	370
Qy	318	ArgGlyValGlyAspLysGlySerSerHisIleLysProLysAlaThrGlySerThr	337
Db	1191	AGAGTGTGTGGGACAAAGGTTTCATCCAGTCAATTAACCAAGGCTTACGAG	390
Qy	338	SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerVal	356
Db	1251	TCAGACCTTGAATAGAAACAGATCTGAATATTTATATACCTTAAATGGGT	410
Qy	357	AspSerGlnProGlnSerLysSerLysAsnThrTyrIleAspGluValAlaGluAsp	376
Db	1311	GACTCACACCAACATCCAAATCAAAAATACATGTTGATGAAAGTTGCAGAG	430
Qy	377	ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln	396
Db	1371	CCTGCAAAATCTCTTACAGAGATATCTACAGACTTTGACCGTCTTCCACC	450
Qy	397	ProProValAsnSerLeuThrGluAsnArgPheHisSerLeuProPheSerLeu	416
Db	1431	CCTCCTCTGTGAACCTCACTGACCCGAGAACAGATTCCACTCTTTACCAT	470
Qy	417	ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuAlaGln	436
Db	1491	ACCAAGATGCCAATACCAATGGAGATTTGGCCACAGTCCACTTTCTCTG	490
Qy	437	SerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro	456
Db	1551	TCTGTAATGGAAGAGCTAAACACTGCACCCGCTCCAAAGAGAGTCCACCT	510
Qy	457	ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro	476
Db	1611	CCTGGAACTCACATGGTCTAGAAAGTGGGCTCATTTGGCTGAAGTTAAG	530
Qy	477	PheTyrGlyValIleArgTyrIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly	496
Db	1671	TTCTATGGGTAATCCGTTGGATCGTCCAGCCACAGAGCTGAATGAAGT	550
Qy	497	LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr	516
Db	1731	CTGGAACCTGGAAGATGAGTGTGAGGCTGTACGATGGAACCTTCAGAG	570
Qy	517	PheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSer	536
Db	1791	TTACCTGTGCTTGAAGAGGCGCTGTGTGAAACTGAAGAGCTGACGAGCT	590
Qy	537	ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe	556
Db	1851	AGGTTTGCATCATTTGACGCGGTTTCCAAATCAGATTGAGCGCTGTAAC	610
Qy	557	GlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGly	576
Db	1911	GGAGGCTACTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGG	630
Qy	577	LeuGluIleMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu	596
Db	1971	TTGAGATATATGATTGGGAAGAAAGGATCCAGGCTCATTAATTTCTT	650
Qy	597	AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg	616
Db	2031	GACTCAACCTTATTTCTGCTTATTTTGTAGTTTCTGTTTGGACACTGT	670
Qy	617	ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu	636
Db	2091	CCCAAGAAACACAGATGATGATATATATAGTGAACCCAGAGACTACT	690
Qy	637	IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg	656
Db	2151	ATTGTTAATCTCTGAGATATATGATATGATGTGTGTCACCAAAATTT	710
Qy	657	LysIleLeuGluLysValGluAlaAlaSerGlyPheThrSerGluGluLysAspProGlu	676

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Db 2211 AANAATCTTGAAGAGTGGAGGCTGCATCAGATTATACCTCTGAAGAAAAAGATCCCTGAG 2270
Qy 677 GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArg 696
Db 2271 GAATCTTGTAATATTCTGTTTCATCATATTTAAGGGTAGAACCTTTTGCTAAAAATAAGA 2330
Qy 697 SerAlaGlyGlnLysValGlnAspCysPheTyrGlnIlePheMetGluLysAsnGlu 716
Db 2331 TCAGCAGGTCAAAAGGTACAAGATTGTTACTTCTATCAAAATTTTATGGAAAAAATGAG 2390
Qy 717 LysValGlyValProThrIleGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeu 736
Db 2391 AAAGTTGGCGTCCCAATTCACAGCTGTGTAGATGGTCTTTTATCAACAGTAACCTG 2450
Qy 737 LysPheAlaGluLaProSerCysLeuIleGlnMetProArgPheGlyLysAspPhe 756
Db 2451 AAATTTGACAGGACCATCATGTCTGATTATTCAGATGCCCTCGATTTGGAAAAAGACTTT 2510
Qy 757 LysLeuPheLysIlePheProSerLeuGluLeuAsnIleThrAspLeuGluAsp 776
Db 2511 AAATATTTAAAAAATTTTCTCTCTGGAATTAATAATAACAGATTTACTTTGAAGAC 2570
Qy 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr 796
Db 2571 ACTCCACAGACAGTCCCGATATGTGGAGGCTTGCAATGTATGATGCTAGAGAATGCTAC 2630
Qy 797 AspAspProAspIleSerAlaGlyLysIleGlnPheCysLysThrCysAsnThrCln 816
Db 2631 GACGATCCGACATCTCAGCTGGAAAAATCAAGCAGTTTTTGTAAACCTCGCAACACTCAA 2690
Qy 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836
Db 2691 GTCCACCTTCATCCGAGAGGCTGAATCATATAATATAACCATGCTCACTTCCCAAGAC 2750
Qy 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856
Db 2751 TTACCCGACTGGGACTGGAGACACGGCTGCATCCCTTCCGAGAAATATGGAGTTATTGCT 2810
Qy 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876
Db 2811 GTTCTCTGCATAGAAACAACCCACTATGTGCTTTTGTGAAGTATGGGAAGGACGATCT 2870
Qy 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896
Db 2871 GCTGGCTCTCTTTTGACAGATGCCGATGGGATGGTGGTCAAGATGGCTTCAACATT 2930
Qy 897 ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu 916
Db 2931 CCTCAAGTCAACCCATGCCAGAGTAGGAGAGTACTTTGAAGATGCTCTGGAGAGACTG 2990
Qy 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936
Db 2991 CATTCCTTGACTCCAGGAGATCCAAAGGCTGTGCACGAGACTGCTTTGTGATGCATAT 3050
Qy 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3051 ATGTGATGTATACCAGAGTCCAAACAATAGATTGTGACAA 3089
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## RESULT 3

US-09-315-788-1729

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; Sequence 1729, Application US/09315788
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; TITLE OF INVENTION: HUMAN ASTROCYTE LIBRARY
; FILE REFERENCE: MLN98-19PM
; CURRENT APPLICATION NUMBER: US/09/315,788
; PUBLICATION DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 60/086,455
; EARLIER PRIORITY DATE: 1998-05-22
; EARLIER APPLICATION NUMBER: 60/132,067
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; EARLIER FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 2346
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1729
; LENGTH: 4664
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(4664)
; OTHER INFORMATION: n = A,T,C or G
US-09-315-788-1729

Alignment Scores:
Pred. No.: 0 Length: 4664
Score: 4983.00 Matches: 948
Percent Similarity: 99.48% Conservative: 0
Best Local Similarity: 99.48% Mismatches: 1
Query Match: 98.99% Indels: 4
DB: 23 Gaps: 4

US-09-671-687A-3 (1-949) x US-09-315-788-1729 (1-4664)
```

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Qy 1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIle 20
Db 230 ATGAGTTTCAGGCTTATGGAGCCAAAGAAAAAGTCACTTCACCTACTGGGAGAGCGGATT 289
Qy 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLys 40
Db 290 TTTTACTTGTCTTCTTCAAGAAATGCAGCGTTACAGACAAACAAACAAAGCTCTCTAAA 349
Qy 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db 350 GTACCGAAGGAAGTATAGGACAGTATATTCAGATTCGTTCTGTGGGCGATTCAAGGATT 409
Qy 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80
Db 410 CCTTCTCAAAAGCAAGAAAAATCAGATTGGATTAAAAATTTAGAGCAACCTCATGCA 469
Qy 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99
Db 470 GTTCTCTTGTGATGAAAGGATGTTGTAGAGATAAATGAAAGTTTACAGAGTTACTTT 529
Qy 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db 530 TTGGCAATTAACCAATTGTGAGAGAGAGGTTACGCTGTTTAAAAACAGAAAAACAGATAAGT 589
Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
Db 590 AAAGGCTCCAAATAGACGTGGGCTGTCCTGTGAAAGTACAGCTGAGATCTGGGAGAGAA 649
Qy 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
Db 650 AAATTTCTGGAGTTGTACGCTTCAGAGGACCCCTGTTAGCAGAGAGACAGTCTCCGGA 709
Qy 160 IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal 179
Db 710 ATATTCTTGGAGTTGAATTGCTGGAAGAGGTCGTGTCGTCGTCGTCGTCGTCGTCGTCG 769
Qy 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db 770 TACCAAGGAAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTGTTCATTTGAC 829
Qy 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
Db 830 AAGCTAGAACTCATAGAAGATGATGACACTGCACTTGGAAAGTATGATACGAGGTCCTGGG 889
Qy 219 AspThrMetGlnValGluLeuProLeuGluLeuAsnSerArgValSerLeuLysGly 238
Db 890 GACCAATGCAAGTTCGAACTTCTCTTCTTGGAAATAAATCACTCAGAGTTTCTTTGAAGGTT 949
Qy 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
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Db 950 GGAGAAACAATAGTAATCTGGACAGTTATATCTGTGATGTTTGGCCAGGAAAAAGAAC 1009  
Qy LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278  
Db 1010 TTAGGATATTTTGTGTGTGGACATGGATTAACCTTATTGGCAACTGGGATGGAGATTT 1069  
Qy 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297  
Db 1070 GATGGAGTCGAGCTTTGTAGTTTGGCGTGTCTGAAAGTAGCAATCTTATTGACATCAAT 1129  
Qy 298 AspileleProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSer 317  
Db 1130 GATATATCCAGAGAGTGTGACCCAGAAAGAGGCTCCCAAACCTTGGCTTTATGTCA 1189  
Qy 318 ArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThr 337  
Db 1190 AGAGTGTGGGGAACAAGTTCTATCCAGTCATTAATAACCAAGGCTACAGGATCTACC 1249  
Qy 338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356  
Db 1250 TCAGACCTCGAATAGAAACAGATCTGAATTTATTTATATCTTAAATGGGTCTCTGTT 1309  
Qy 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376  
Db 1310 GACTCACACCAACCAATCAAAATCAAAATAACATGGTACATTTGATGAAGTTGCAAGAC 1369  
Qy 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln 396  
Db 1370 CCTGCAAAATCTTTACAGAGATATCTACAGACTTTTGACCGTTCTTCCACCACCTCCAG 1429  
Qy 397 ProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416  
Db 1430 CCTCTCTCTGTAACCTACTGACCACCGAGNACAGATTCCACTCTTTACCAATCAGTCTC 1489  
Qy 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436  
Db 1490 ACCAAGATGCCAATACCAATGGAAGTATTGGCCACAGTCCACTTTCTCTGACGCCAG 1549  
Qy 437 SerValMetGluLeuLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro 456  
Db 1550 TCTGTATGGAAGAGCTTAACACTGCAACCGCTCCAGAGAGTCCACCGTTGGCCATCGCT 1609  
Qy 457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476  
Db 1610 CCTGGAACTCACATGCTAGAAAGTGGGCTCATTTGGCTGAAGTTAAGGAGAACCTCTCT 1669  
Qy 477 PheTyrGlyValIleArgTTPilleGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496  
Db 1670 TTCTATGGGGTAATCCGGTTGGATCGGTGAGCCACAGGACTGAATGAAGTCTCGCTGA 1729  
Qy 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516  
Db 1730 CTGGAACCTGGAAGATGAGTGTGAGGCTGTACGGATGGAACCTTCAGAGGCACTCGGTAT 1789  
Qy 517 PheThrCysAlaLeuLeuLysAlaLeuPheValLysLeuLysSerCysArgProAspSer 536  
Db 1790 TTCACTGTGCCCTGAAGAGCCCTGTTTGTGAACCTGAAGAGCTGACGCTGACTCT 1849  
Qy 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556  
Db 1850 AGGTTTGATTCATTCGACCGCGTTTCCAATCAGATTGAGCGCTGTAACTCTTTAGCAAT 1909  
Qy 557 GlyGlyTyrLeuSerGluValValGluAsnThrProProLysMetGluLysGluGly 576  
Db 1910 GGAGGCTACTTAAAGTGAAGTAGTAGAGAAATACTCCACCAAAATGGAAGAGAGGC 1969  
Qy 577 LeuGluIleMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596  
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Qy 597 AspSerThrLeuPheCysLeuPheAlaPheSerValLeuAspThrValLeuLeuArg 616  
Db 2030 GACTCAACCTTATCTGCTTATTTGCTTTTAGTTCTGTTCTGGACACTGTCTTACTTACA 2089

Qy 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636  
Db 2090 CCCAAAGAAAGAACGATGATAGATATTTATAGTGAACCCCAAGAGCTACTGAGGACAGAA 2149  
Qy 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656  
Db 2150 ATTGTTAATCTCTGAGAAATATATGATGATGTTGTGTGCCACAAAATTTATGAACTGAGG 2209  
Qy 657 LysIleLeuGluLysValGluAlaSerGlyPheThrSerGluGluLysAspProGlu 676  
Db 2210 AAAATACTTGAAGAGGTGGAGCTGCATCAGGATTTACCTCTGAAGAAAAAGATCCTGAG 2269  
Qy 677 GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArg 696  
Db 2270 GAATCTCTGAATATCTGTTTCATCATATTTTAAGGTAGAACCTTTGCTAAAAATAGA 2329  
Qy 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716  
Db 2330 TCAGCAGGTCAAAAGGTACAAGATTGTTACTTCTATCAAAATTTTATGAAAAAATGAG 2389  
Qy 717 LysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeu 736  
Db 2390 AAAGTTGGCGTTCCCAAAATTCAGCAGTTGTAGAAATGCTCTTTTATCAACAGTAACCTG 2449  
Qy 737 LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPhe 756  
Db 2450 AAATTTGCAGAGGACCAATCATGTGATTAATTCAGATGCCCTCGATTTGGAAAAACCTTT 2509  
Qy 757 LysLeuPheLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAsp 776  
Db 2510 AAACCTATTTAAAAAATTTTTCTCTCTGAAATTAATAATAACAGATTACTTGAAGAC 2569  
Qy 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr 796  
Db 2570 ACTCCAGACAGTCCGGATATGTGGAGGCTTGCAATGTATGATGATGATGATGATGATGAT 2629  
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Db 2630 GACCATCCGACATCTCAGCTGGAAAAATCAAGCAGTTTGTAAAAACCTGCACACTCAA 2689  
Qy 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836  
Db 2690 GTCCACCTTCATCCGAAGAGGCTGAATCATATAATAACCCAGTGTCTACTTCCCAAGAC 2749  
Qy 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856  
Db 2750 TTACCCGACTGGGACTGGAGACACGGCTGCATCCCTTGCAGAAATATGGAGTTATTTGCT 2809  
Qy 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876  
Db 2810 GTTCTCTGCATAGAAACCAAGCCACTATGTTGTTTGTGAAGTATGGGAAGGACCAATCT 2869  
Qy 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896  
Db 2870 GCCTGGCTCTCTTTGACAGCATGGCCGATCGGATGTTGGTTCAGATGGCTTCAACATT 2929  
Qy 897 ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu 916  
Db 2930 CCTCAAGTCACCCCATGCCAGAGTAGGAGACTTGAAGATGCTCTGGAAGACCTG 2989  
Qy 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936  
Db 2990 CATTCCTTGGACTCCAGAGAAATCAAGGCTGTGCACGAAGACTGCTTTGTGATGCATAT 3049  
Qy 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949  
Db 3050 ATGTGATGTACAGAGTCCAAATGATGTTTGTACAAA 3088

## RESULT 4

US-09-315-788A-1729

; Sequence 1729, Application US/09315788A

; GENERAL INFORMATION:

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; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; TITLE OF INVENTION: HUMAN ASTROCYTE LIBRARY
; FILE REFERENCE: 1600.1019-002
; CURRENT PUBLICATION NUMBER: US/09/315,788A
; CURRENT PUBLICATION DATE: 2009/05/21
; PRIOR APPLICATION NUMBER: 09/315,788
; PRIOR APPLICATION DATE: 2009/05/21
; PRIOR APPLICATION NUMBER: 60/086,455
; PRIOR APPLICATION DATE: 1998/05/22
; PRIOR APPLICATION NUMBER: 60/132,067
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 2346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1729
; LENGTH: 4664
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4664)
; OTHER INFORMATION: n = A, T, C or G
US-09-315-788A-1729

Alignment Scores:
Pred. No.: 0 Length: 4664
Score: 4983.00 Matches: 948
Percent Similarity: 99.48% Conservative: 0
Best Local Similarity: 99.48% Mismatches: 1
Query Match: 98.99% Indels: 4
DB: 23 Gaps: 4

US-09-671-687A-3 (1-949) x US-09-315-788A-1729 (1-4664)

QY 1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIle 20
DB 230 ATGAGTTTCAGGCTTATGGAGCCCAAGAAAGTCACTTCCCTTACTGGGAAGCGGATT 289
QY 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40
DB 290 TTTTACTTGTCTTCAAGAAATGACGTTTACAGACAAACAAACAAAGCTCCCTTAA 349
QY 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
DB 350 GTACCGAAGGAGTATAGACAGTATATTCAGATCTTCTCTGGGCAATTCAGGATT 409
QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnProHisAla 80
DB 410 CCTTCTGCAAAAGCAAGAAATACAGATTGGATTAAATTTCTAGAGCAACCTCATGCA 469
QY 81 ValLeuPheValAspGlu---AspValValGluLysValThrGlnLeuLeu 99
DB 470 GTTCTCTTTTGTGATGAAAGGATGTTGTAGATATAATGAAAGTTTACAGATTACTT 529
QY 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgLeuSer 119
DB 530 TTGGCAATTTACCAATTTGTGAGGAGAGTTTCCAGCTGTTTAAACACAGAACTAAGT 589
QY 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGlu 139
DB 590 AAAGGCTCCAAATAGACGTGGGCTGCTCTGTGAAAGTACAGCTGAGATCTGGGGAGAA 649
QY 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
DB 650 AAATTTCTGAGTTGTACGCTTTCAGAGGACCCCTGTTAGCAGAGGACAGTCTCCGGA 709
QY 160 IlePhePheGlyValGlnLeuLeuGluGlyArgGlyGlnGlyPheThrAspGlyVal 179
DB 710 ATATTCTTTGGATTGAATTTGCTGGAGAGGCTGCTGGTCAAGGTTTCACTGACGGGGT 769
QY 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
DB 1850 AGGTTTGCATCATTTGACGCGGTTTCCAAATCAGATTGACGCTGTAACCTTTTAGCATTT 1909

770 TACCAAGGGAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTTGTGATGGAC 829
199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
830 AAGCTAGAACTCATAGAAAGATGATGACACTGCATTGGAAGATGATTACGACGCTCTGG 889
219 AspThrMetGlnValGluLeuProProLeuGluLysLeuSerArgValSerLeuLysGly 238
890 GACCAATGCGAGTGCAGACTTCTCTCTTGGAAATAAACTCCAGAGTTTCTTTTGAAGTT 949
239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
950 GGAGAAACAATAGAAATCTGGAAACAGTTATATCTGTGATGTTTTCGCCAGGAAAGAAC 1009
259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
1010 TTAGGATATTTGTTGGTGGACATGATTAACCTATTGGCAACTGGGATGAAGATTT 1069
279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
1070 GATGAGTGCAGCTTCTGTAGTTTTCGCTGTCTGAAAGTACAAATCTATTGACATCAAT 1129
298 AspIleIleProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSer 317
1130 GATATCATCCAGAGAGTGTACGAGAAAGGAGGCTCCCAAACTTGCCTTTATGTCA 1189
318 ArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThr 337
1190 AGAGTGTGTTGGGCAAAAGTTTCATCCAGTCAATAATAAACCAAGGCTTACAGATCTACC 1249
338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356
1250 TCAGACCTTGGAAATAGAAACAGATCTGAATTTATTTATACCTTAAATGGGTCTTCTGT 1309
357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376
1310 GACTCACACACAAATCCAAATCAAAATAATACATGTTGATGATGAAAGTTGCAGAGAC 1369
377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProLeuGln 396
1370 CCTGCAAAATCTCTTACAGAGATATCTACAGACTTTTGACCGTCTTTCACCACTCCAG 1429
397 ProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416
1430 CCTCTCTCTGAACTCACTGACCAACAGAGACAGATTCACACTCTTTACCAATTCAGTCTC 1489
417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436
1490 ACCAAGATGCCAATACCAATGGAAGTATTGGCCACAGTCCACTTCTCTGTGAGCCAG 1549
437 SerValMetGluLeuLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro 456
1550 TCTGTATGGAAGAGCTTAAACACTGACCCCGCTCAAGAGAGTCCACCTTGGCCATGCT 1609
457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476
1610 CCTGGGAACTCACATGCTTAGAAGTGGCTCAITGCTGAAGTTAAGAGAACCTCTCT 1669
477 PheTyrGlyValIleArgTyrIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496
1670 TTCTATGGGTAAATCCGTTGGATCGGTGACCCAGGAGTGAATGAAGTGTCTGCTGGA 1729
497 LeuGlnLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516
1730 CTGGAACCTGGAAGATGATGTGACAGGCTGTACGATGGAACCTTTCAGAGGACCTCGGTAT 1789
517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLysSerCysArgProAspSer 536
1790 TTCACCTGTCCCTGGAAGAGGCGCTGTTGTGAAACTGAAGAGCTGACGCGCTGACTCT 1849
537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556
1850 AGGTTTGCATCATTTGACGCGGTTTCCAAATCAGATTGACGCTGTAACCTTTTAGCATTT 1909
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Qy 557 GlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGly 576  
Db 1910 GGAGGCTACTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATCGAAAAAGAGGC 1969  
Qy 577 LeuGluileMetileGlyLysLysGlyileGlnGlyHisTyrAsnSerCysTyrLeu 596  
Db 1970 TTGGAGATAATGATTTGGGAAGAAAGGAGCTCCAGGGTCAATTAATTTCTTTACTTA 2029  
Qy 597 AspSerThrLeuPheCysLeuPheAlaPheSerValLeuAspThrValLeuLeuArg 616  
Db 2030 GACTCAACCTTATCTGCTTATTTGCTTTTAGTTCTGTTCTGGACACTGGTTACTTAGA 2089  
Qy 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636  
Db 2090 CCCAAAGAAAGAACGATGATAGATATATAGTGAACCCCAAGAGCTACTGAGGACAGAA 2149  
Qy 637 IleValAsnProLeuArgileTyrGlyTyrValCysAlaThrLysileMetLysLeuArg 656  
Db 2150 ATTGTTAATCCTCTGAGATATATGATATGTTGTGTGCCACAAATTTATGAACTGAGG 2209  
Qy 657 LysileLeuGluLysValGluAlaSerClyPheThrSerGluGluLysAspProGlu 676  
Db 2210 AAAATCTTGAAAGGTTGAGGCTGCATCAGGATTTACCTCTGAAGAAAAAGATCCTGAG 2269  
Qy 677 GluPheLeuAsnileLeuPheHisileLeuArgValGluProLeuLeuLysileArg 696  
Db 2270 GAATCTTGATATCTGTTTCATCATATTTTAAAGGTAGAACCTTTGCTTAAAAATAGA 2329  
Qy 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnilePheMetGluLysAsnGlu 716  
Db 2330 TCAGAGCTCAAAAGGTACAGATTTGTTACTTCTATCAAAATTTTATGGAATAAATAGAG 2389  
Qy 717 LysValGlyValProThrileGlnGlnLeuLeuGluThrPhePheileAsnSerAsnLeu 736  
Db 2390 AAAGTTGCGCTTCCCAAAATTCAGCAGTTGTAGAAATGGTCTTTTATCAACAGTAACCTG 2449  
Qy 737 LysPheAlaGluAlaProSerCysLeuileileGlnMetProArgPheGlyLysAspPhe 756  
Db 2450 AAATTTGCAGAGGACCATCATGCTGATATATCAGATGCTCGATTTGGAAAGACTTT 2509  
Qy 757 LysLeuPheLysLysilePheProSerLeuLeuAsnileThrAspLeuLeuGluAsp 776  
Db 2510 AAACATTTTAAAAAATTTTCTCTCTGGAATTTAAATATAACAGATTTACTTTGAAGAC 2569  
Qy 777 ThrProArgGlnCysArgileCysGlyLeuAlaMetTyrGluCysArgGluCysTyr 796  
Db 2570 ACTCCAGACAGTCCGATATGTGAGGGCTTGAATGTATGATGCTAGAGATGCTAC 2629  
Qy 797 AspAspProAspIleSerAlaGlyLysileLysGlnPheCysLysThrCysAsnThrGln 816  
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Qy 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836  
Db 2690 GTCCACCTTCATCCGAAGGCTGAATCAATATAATACCAGTGTCACTTCCCAAGAC 2749  
Qy 837 LeuProAspTrpAspTrpArgHisGlyCysileProCysGlnAsnMetGluLeuPheAla 856  
Db 2750 TTACCCGACTGGGACTGGAGACACGGCTGCATCCCTTGGCAGATATGAGTATTTGCT 2809  
Qy 857 ValLeuCysileGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876  
Db 2810 GTTCTCTGCATAGAAACAAGCACTATGTTGCTTTTGTGAAGTATGGAAGGACGATCT 2869  
Qy 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnile 896  
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Db 2930 CCTCAAGTCCACCCATGCCAGAGTAGGAGAGTACTTGAAGATGTCTCTGGAAGACCTG 2989

Qy 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936  
Db 2990 CATTCCTTGGACTCCAGAGAATCCAGGCTGTGCACGAAGACTGCTTTGTGATGCATAT 3049  
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RESULT 5  
US-09-783-514-1729  
; Sequence 1729, Application US/09783514  
; GENERAL INFORMATION:  
; APPLICANT: Gearing, David P.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A  
; TITLE OF INVENTION: HUMAN ASTROCYTE LIBRARY  
; FILE REFERENCE: 1600.1019-002  
; CURRENT APPLICATION NUMBER: US/09/783,514  
; CURRENT FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: 09/315,788  
; PRIOR FILING DATE: 1999-05-21  
; PRIOR APPLICATION NUMBER: 60/086,455  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/132,067  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 2346  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1729  
; LENGTH: 4664  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(4664)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-783-514-1729  
Alignment Scores:  
Pred. No.: 0 Length: 4664  
Score: 4983.00 Matches: 948  
Percent Similarity: 99.48% Conservative: 0  
Best Local Similarity: 99.48% Mismatches: 1  
Query Match: 98.99% Indels: 4  
DB: 32 Gaps: 4  
US-09-671-687A-3 (1-949) x US-09-783-514-1729 (1-4664)  
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Qy 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40  
Db 290 TTTTACTTGTCTTCTTCAAGATGCGGTACAGACAAACAAACACAAAGCTCCTTAAA 349  
Qy 41 ValProLysGlySerileGlyGlnTyrileGlnAspArgSerValGlyHisSerArgile 60  
Db 350 GTACCGAAGGAGGATATAGGACAGTATATCAAGATCGTCTGTGGGCATTCAAGGATT 409  
Qy 61 ProSerAlaLysGlyLysLysAsnGlnileGlyLeuLysileLeuGluGlnProHisAla 80  
Db 410 CCTTCTGCAAAAGGACAGAAAAATCAGATTGGATTAAAAATCTAGAGCAACCTCATGCA 469  
Qy 81 ValLeuPheValAspGlu---AspValValGluileAsnGluLysPheThrGluLeuLeu 99  
Db 470 GTTCTCTTTGTTGATGAAAAGGATGTTGTAGAGATAAATGAAAGCTTCACAGATTACTT 529  
Qy 100 LeuAlaileThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119  
Db 530 TTGGCAATTTACCAATTTGTGAGGAGGTTTCAGCCTGTTTAAAAACAGAAACAGACTAAGT 589  
Qy 120 LysGlyLeuGlnileAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139



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QY 160 IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal 179  
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QY 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly--PheValAlaLeuAsp 198  
Db 770 TACCAGGGGAAAAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTGTGCAATGGAC 829  
QY 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218  
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Db 890 GACACAATGCAGGTCCAACTTCCTCTTTGGAAATAAACTCCAGAGTTTCTTTGAAGGTT 949  
QY 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258  
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QY 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278  
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QY 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297  
Db 1070 GATGGAGTCAGCTTTGTAGTTTGGCTGTGTGTTGAAAGTACAATTTCTATTGCACATCAAT 1129  
QY 298 AspilelleProGluSerValThrGlnGluArgArgProProLysLeuAlaPheMetSer 317  
Db 1130 GATATCATCCAGAGAGTGTGACGCAAGGAAAGAGGCGCTCCCAAACTTGCCTTTATGTCA 1189  
QY 318 ArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThr 337  
Db 1190 AGNGTGTGGGGACAAAGGTTTCATCCAGTCATATAATAACCAAGGCTACAGATCTACC 1249  
QY 338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356  
Db 1250 TCAGACCCCTGGAAATAGAAACAGATCTGAATTTATTTATACCTTAAATGGGTCTCTGTT 1309  
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Db 1310 GACTCACACCAACCAATCCAAATCAAAAATACATTTGATGATGAAAGTTGCAGAAGAC 1369  
QY 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerProProLeuGln 396  
Db 1370 CTGCAAAATCTTTACAGAGATATCTACAGCTTTTGACCGTTCCTCACCAACCTCCAG 1429  
QY 397 ProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416  
Db 1430 CCTCTCTCTGTGAACCTCACTGACCAACCGAGAACAGATTCCACTCTTTACCAATTCAGTCTC 1489  
QY 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436  
Db 1490 ACCAAGATGCCAAATACCAATGGAAGTATTGGCCACAGTCCACTTCTCTGTCTGAGCCAG 1549  
QY 437 SerValMetGluLeuLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro 456  
Db 1550 TCTGTAATCGAAGAGCTAAACACTGACCCCGTCCAAAGAGAGTCCACCTTGGCCATGCCT 1609  
QY 457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476  
Db 1610 CTGGGAACCTACATGGCTTAGAAGTGGGCTCATTTGGCTGAAGTTAAGGAGAACCTCTCT 1669  
QY 477 PheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496  
Db 1670 TTCTATGGGTATTCGGTTGGATCGGTACGCCACCAAGGACTGNAATGAAGTGTCTCGTGG 1729

QY 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516  
Db 1730 CTGGAATCGGAAGATGAGTGTGAGGCTGTACGGATGGAACCTTCAGAGGCACTCGGTAT 1789  
QY 517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLysLeuLysSerCysArgProAspSer 536  
Db 1790 TTCACTGTGCTCCCTGGAAGAGGCGCTGTTGTGAAACTGAAAGAGCTGCAGGCTGACTCT 1849  
QY 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556  
Db 1850 AGTTTGCATCATTTGCAGCGGTTTCCATCAGATTGAGCGCTGTAACTCTTTAGCATTT 1909  
QY 557 GlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGly 576  
Db 1910 GGAGGCTACTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAAGAGAGGC 1969  
QY 577 LeuGluIleMetIleGlyLysLysGlyGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596  
Db 1970 TTGGAGATAATGATTGGGAAGAGAAAGGCAATCCAGGGTCAATTACAAATCTTGTACTTA 2029  
QY 597 AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg 616  
Db 2030 GACTCAACCTTATCTCTCTTATTTAGTTCTGTCTGTGACACTGTGTACTTAGA 2089  
QY 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636  
Db 2090 CCCAAAGAAAAGAACGATGTAGATAATTATAGTGAACCCCAAGAGCTACTGAGGACAGAA 2149  
QY 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656  
Db 2150 ATTTGTTAATCTCTGAGATATATGGATATGTGTGTGCACAAAAATATGAAACTGAGG 2209  
QY 657 LysIleLeuGluLysValGluAlaAlaSerGlyPheThrSerGluGluLysAspProGlu 676  
Db 2210 AAAATACTTGAAGAGGTGGAGGTGCATCAGGATTTTACCTCTGAAGAAAAAGATCCTCAG 2269  
QY 677 GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArg 696  
Db 2270 GAATTTCTGATATATCTGTTTTCATCATATTTAAGGGTAGAACCTTTGCTAAAAATAAGA 2329  
QY 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716  
Db 2330 TCAGCAGGTCAAAAGGTACAAAGATTGTTACTTCTATCAAAATTTTATGGAAAAAATGAG 2389  
QY 717 LysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeu 736  
Db 2390 AAAAGTTGGCGTTCCCAATTCAGCAGTTGTTAGAATGGTCTTTTATCAACAGTAACCTG 2449  
QY 737 LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPhe 756  
Db 2450 AAAATTTGCAGAGCACCATCATGTCTGATTTATCAGATGCTCGATTTGGAAAAAGACTTT 2509  
QY 757 LysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAsp 776  
Db 2510 AAATAATTTAAAAAATTTTCTCTCTCGAATTAATAATAACAGATTTTACTTGAAGAC 2569  
QY 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr 796  
Db 2570 ACTCCAGACAGTCCCGGATATGTGGAGGCGTTGCAATGTATGAGTGTAGAGAATGCTAC 2629  
QY 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln 816  
Db 2630 GACGATCCGAGACTCTCAGCTGGAAAAAATCAAGCAGTTTTTGTAAAAACTCGCAACACTCAA 2689  
QY 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836  
Db 2690 GTCCACTTCATCCGAAAGAGGCTGAATCATATAATATAAACCCAGTGTCACTTCCCAAGAC 2749  
QY 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856  
Db 2750 TTACCCGACTGGGACTGGAGACACGGCTGCATCCCTTGGCCAGATATGGAGTTATTTGCT 2809



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QY 437 SerValMetGluGluLeuLeuAsnThrAlaProValGlnGlnSerProProLeuAlaMetPro 456
Db 1550 TCTGTAATGAAGAGCTAAACACTGCAACCCGCTCCAGAGAGTCCACCCCTTGCCATGCCT 1609
QY 457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476
Db 1610 CCTGGGAACCTCACAATGCTCAGAGTGGGCTCATTTGGCTGAAGTTAAGGGAACCCCTCT 1669
QY 477 PheTyrGlyValIleArgTTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496
Db 1670 TTCTATGGGGTAATCCGTTGGATCGGTGAGCCACAGGACTGAATGAAGTGTCTCGCTGGA 1729
QY 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516
Db 1730 CTGGAACCTGAAGATGAGTGTGAGGCTGTACGGATGGACCTTCAGAGGCACTCGGTAT 1789
QY 517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSer 536
Db 1790 TTCACCTGTCCCTGGAAGAAGGGCTGTTTGTGAAACTGAAGAGCTGCAGGCTGACTCT 1849
QY 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556
Db 1850 AGGTTTGCATCATTTGACGCGGCTTCCCAATCAGATTGAGCGCTGTAACTCTTTAGCAATTT 1909
QY 557 GlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGly 576
Db 1910 GGAGGCTACTTAAGTAGAGTAGTAGAAGAAATACTCCACCAAAATGGAAAAGAGGC 1969
QY 577 LeuGluIleMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596
Db 1970 TTGGAGATTAATGATTGGGAAGAAGAGGCAATCCAGGGTCAATACAACTCTTGTACTTA 2029
QY 597 AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg 616
Db 2030 GACTCAACCTTATCTGCTTATTTGCTTTTGTGTTTCTGTTCTGACACTGTGTTACTTGA 2089
QY 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636
Db 2090 CCCAAAGAAAAGAACCATGTAGAAATATATATAGTAAACCCCAAGAGCTACTGAGGACAGAA 2149
QY 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656
Db 2150 ATTGTTAACTCTGAGATATATATGATATGTGTGTGCCCAAAAATTTATGAACCTGAGG 2209
QY 657 LysIleLeuGluLysValGluAlaAlaSerGlyPheThrSerGluGluLysAspProGlu 676
Db 2210 AAAATACTTGAAGGTGGAGGCTGCATCAGGATTTACCTCTGAAGAAAAGATCCTGAG 2269
QY 677 GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArg 696
Db 2270 GAATCTTGAATATTCTGTTTCATCATATTTTAAAGGTAGAACCCTTTGCTAAAAATAAGA 2329
QY 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716
Db 2330 TCAGCAGGTCAAAAGGTACAAGATTGTTACTTCTCAAAATTTTATGGAAGAAAATGAG 2389
QY 717 LysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeu 736
Db 2390 AAAGTTGGGGCTTCCCAACAATTCAGCAGTGTGTAGAATGGTCTTTTATCAACAGTAACCTG 2449
QY 737 LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPhe 756
Db 2450 AAATTTGAGAGGCACCATCATGCTGATATTATTCAGATGCTCGATTTTGGAAAAGACTTT 2509
QY 757 LysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAsp 776
Db 2510 AAACATTTTAAAAAATTTTCTCTCTCGGAATTAATAATAACAGATTTTACTTTGAAGAC 2569
QY 777 ThrProArgGlnCysArgIleCysGlyLeuAlaMetTyrGluCysArgGluCysTyr 796
Db 2570 ACTCCAGACAGTCCGGATATGTGGAGGCTTGCAATGTATGAGTGTAGAGAATGCTAC 2629
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QY 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln 816
Db 2630 GACGATCGGACATCTCAGCTGGAAAAATCAAGCAGATTGTTGAAAACCTGCAACACTCAA 2689
QY 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836
Db 2690 GTCCACCTTTCATCCGAAGAGGCTGAATCATAAATATAACCCAGTGTCACTTCCCAAGAC 2749
QY 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856
Db 2750 TTACCCGACTGGGACTGGAGACACGGCTGCATCCCTTCCAGATATGGAGTTATTGCT 2809
QY 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspSer 876
Db 2810 GTTCTCTGCATAGAAACAAGCCACTATGTTGCTTTTGTGAAGTATGGGAAGCAGCATTTCT 2869
QY 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896
Db 2870 GCCTGGCTCTTCTTTGACAGCATGCCGATCGGATGGTGGTCAAGATGGCTTCAACATT 2929
QY 897 ProGlnValThrProCysProGluValGlyGluTyrIleLysMetSerLeuGluAspLeu 916
Db 2930 CCTCAAGTCAACCCATGCCAGAAAGTAGAGAGTACTTTGAAGATGCTCTTGGAGACCTG 2989
QY 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936
Db 2990 CATTCCTTGGACTCCAGAGAAATCCAGGCTGTGCACGAAGACTCTTTGTGATGCATAT 3049
QY 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3050 ATGTGCATGTACCAGAGTCCCAACATGAGTTGTACAAA 3088
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## RESULT 7

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US-09-396-087-4309
; Sequence 4309, Application US/09396087
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; TITLE OF INVENTION: PULMONARY ARTERY SMOOTH MUSCLE LIBRARY
; FILE REFERENCE: MLN98-39PM
; CURRENT APPLICATION NUMBER: US/09/396,087
; CURRENT FILING DATE: 1999-09-14
; EARLIER APPLICATION NUMBER: 60/100,260
; EARLIER FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: 60/107,226
; EARLIER FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: 60/131,810
; EARLIER FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5220
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4309
; LENGTH: 4668
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(4668)
; OTHER INFORMATION: n = A,T,C or G
US-09-396-087-4309
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## Alignment Scores:

Pred. No.:	0	Length:	4668
Score:	4903.00	Matches:	948
Percent Similarity:	99.48%	Conservative:	0
Best Local Similarity:	99.48%	Mismatches:	1
Query Match:	98.99%	Indels:	4
DB:	23	Gaps:	4

US-09-671-687A-3 (1-949) x US-09-396-087-4309 (1-4668)

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QY 1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluArgIle 20
|||||
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Db 230 ATGAGTTACGGCTTATGGAGCCAAAGAAAAGTCACTTACCCTACTCGGAGAGCGGATT 289  
Qy 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLys 40  
Db 290 TTTTACTTGCTTCTTCAAGATGTCAGCGTTACAGACAAACAAACAGCTCTTAAA 349  
Qy 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60  
Db 350 GTACCGAAGGGAAGTATAGGACAGTATATTCAAGATCGTTCTGTGGGGCATTTCAAGGATT 409  
Qy 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnProHisAla 80  
Db 410 CCTTCTGCAAAAGCGCAAGAAAATCAGATTGGATTTAAAAATTCAGAGCAACCTCATGCA 469  
Qy 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99  
Db 470 GTTCTCTTTGTTGATGAAAAGGATGTTGTAGAGNTAAATGANAAGTTTCAGAGTTACTT 529  
Qy 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119  
Db 530 TTGGCAATTAACCAATTGTGAGGAGAGTTTCAGCGCTGTTTAAAAACAGAAACAGACTAAGT 589  
Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139  
Db 590 AAAGGGCTCCAAATAGACGTGGGCTGCTCTGTGAAAGTACAGCTGAGATCTGGGGAGAA 649  
Qy 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159  
Db 650 AAATTTCTGGAGTTGTACCGCTTCAGAGGACCCTGTTTACAGAGAGGACAGTCTCCGGA 709  
Qy 160 IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal 179  
Db 710 ATATTCTTTGGAGTTGAAATGCTGGAGAGAGTCTGTGTCAGGTTTCACTGACGGGGTG 769  
Qy 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198  
Db 770 TACCAAGGGGAAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTGTTGCAATGGAC 829  
Qy 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218  
Db 830 AAGCTAAGACTCATAGAAGATGATGACACTGCAATTTGGAAAGTATTAACGAGGTCTCTGGG 869  
Qy 219 AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly 238  
Db 890 GACACAATGAGGTGCAACTCTCTCTTTGGAAATAAACTCCAGAGTTTCTTTGAAGTT 949  
Qy 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258  
Db 950 GGAGAAACAATAGAACTCGAAACAGTTATATTCTGTGATGTTTGGCCAGGAAAGAAAGC 1009  
Qy 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278  
Db 1010 TTAGGATATTTTGTGTGTGGTGGCATGGATAACCCATTATGGCAACTGGGATGGAAAGATT 1069  
Qy 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297  
Db 1070 GATGGAGTGACGCTTTGTAGTTTTCGTTGCGTGTGTAAGAGTCAAAATCTATTGGCACAAT 1129  
Qy 298 AspIleIleProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSer 317  
Db 1130 GATATCATCCAGAGAGTGTGACGAGGAAAGAGGGCTCCCAAACTTGCTTTATGTCA 1189  
Qy 318 ArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThr 337  
Db 1190 AGAGGTGTTGGGACAAAGGTTTCATCAGTCAATAAATAACCAAGGCTACAGGATCTACC 1249  
Qy 338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356  
Db 1250 TCAGACCTCGGAATAGAAAACAGATCGAATATTTTATACCTTAAATGGGCTCTCTGTT 1309  
Qy 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376  
Db 1310 GACTCACACCAACCAATCAAAAATACATGGTACATGGTACATGGTGAAGTTGCAGAGAC 1369

Qy 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln 396  
Db 1370 CCTGCAAAATCTCTTTACAGAGATATCTACAGACTTTGACCGTCTCTTCCACCACCACTCCAG 1429  
Qy 397 ProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416  
Db 1430 CCTCCTCTGTGAACCTCACTGACCACCGAGAACAGATTCCACTCTTTTACCATTCACTCTC 1489  
Qy 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436  
Db 1490 ACCAAGATGCCCAATACCAATGGAAAGTATTGGCCACAGTCCACTTCTCTGTGACCCCG 1549  
Qy 437 SerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro 456  
Db 1550 TCTGTANTGGAGAGCTTAACACTGACCCGCTCCAGAGAGTCCACCCCTTGGCCATGCT 1609  
Qy 457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476  
Db 1610 CCTGGGAACCTCACATGCTTAGAAGTGGGCTCATTTGGCTGAAGTTAAGGAGAACCTCCT 1669  
Qy 477 PheTyrGlyValIleArgTyrIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496  
Db 1670 TTTCTATGGGTAAATCCGTTGGATCGGTGACCCAGCAGACTGAATGAAGTGTCTCTGGA 1729  
Qy 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516  
Db 1730 CTGGAACTGGAAAGTGTGTGACAGGCTGTACGGATGGAACTTTCAGAGGCACTCGGTAT 1789  
Qy 517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSer 536  
Db 1790 TTCACCTGTGCCCTGAAAGAGCGCTGTTTCTGAAACTGAAGAGCTGCAGGCTGACTCT 1849  
Qy 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556  
Db 1850 AGGTTTGCATCATTTGACCGCGTTTCCAATCAGATTGAGCGCTGTAACTCTTTTACATTT 1909  
Qy 557 GlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGly 576  
Db 1910 GGAGGCTACTTTAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAAAAAGAGGC 1969  
Qy 577 LeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596  
Db 1970 TTGGAGATATGATTGGGAAGAGAAAGGCATCCAGGGCTATTACAATTTCTTTTACTTA 2029  
Qy 597 AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg 616  
Db 2030 GACTCAACCTTATTTCTGCTTATTTGCTTTTAGTTCTGTTCTGGACACTGTGTACTTAGA 2089  
Qy 617 ProLysGlyLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636  
Db 2090 CCCAAAGAAAGAACGATGTAGAAATATTATAGTGAACCCCAAGAGCTACTGAGGACAGAA 2149  
Qy 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656  
Db 2150 ATTGTTAATCTCTGAGATATATGATATGTGTGTCACAAATAATTTATGAACTGAGG 2209  
Qy 657 LysIleLeuGluLysValGluAlaAsnArgGlyPheThrSerGluGluLysAspProGlu 676  
Db 2210 AAAATCTTGAAAGGTGGAGGCTGCATCAGATTTTACCTCTGAAGAAAAAAGATCCTCAG 2269  
Qy 677 GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArg 696  
Db 2270 GAATTTCTGAAATATTTCTGTTTCATATATTTTAAAGGTAGAACCTTTGCTAAAAATAAGA 2329  
Qy 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716  
Db 2330 TCAGAGCTCAAAAGGTACAGATTTGTTACTTCTATCAAAATTTTATGGAAAAAATAAGT 2389  
Qy 717 LysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeu 736  
Db 2390 AAAGTTGGCGTTCCCACAATTCAGCAGTTGTTAGAAATGGTCTTTTATCAACAGTAACCTG 2449

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QY 737 LysPheAlaGluAlaProSerCysLeuIleGlnMetProArgPheGlyLysAspPhe 756
DB 2450 AAATTTGAGAGGACCATCATGCTGATTAATCAGATGCGCTCGAATTTGGAAAGACTTT 2509

QY 757 LysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAsp 776
DB 2510 AAACATATTAATAAATTTTCCCTCTCTGGAATTAATAATACAGATTTACTTGAAGAC 2569

QY 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr 796
DB 2570 ACTCCAGACAGTCCCGATATGTGGAGGCTTGCATATGATGATGAGTAGAGATGCTAC 2629

QY 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln 816
DB 2630 GACGATCCGGACATCTCAGCTGGAAAAATCAAGCAGATTTTGTAAACCTGCAACACTCAA 2689

QY 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836
DB 2690 GTCCACCTTATCCGAAGAGGCTGATCATATAATATAATACCCAGTGTCACTTCCCAAGAC 2749

QY 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856
DB 2750 TTACCCGACTGGGACTGGAGACACGGCTGCATCCCTTGGCCAGATATGGAGTTATTTGCT 2809

QY 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876
DB 2810 GTTCTCTGCATAGAAACAAGCCACTATGTTGCTTTTGTGAAGTATGGGAAGCAGATTCT 2869

QY 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896
DB 2870 GCCTGGCTCTTCTTTGACAGATCGCCGATCGGATGCTGTCAGAAATGGCTTCAACATTT 2929

QY 897 ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu 916
DB 2930 CCTCAAGTCAACCATCCAGAGAGTAGGAGACTTGAAGATGTCTCTGSAAGACCTG 2989

QY 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936
DB 2990 CATTCCTTGGACTCCAGGAGAAATCCAAAGGCTGTGCACGAAGACTGCTTTGTGATGCATAT 3049

QY 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
DB 3050 ATGTGCATGTACCAGAGTCCAAACAATGAGTTGTACAAA 3088
```

## RESULT 8

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US-09-396-970-7559
; Sequence 7559, Application US/09396970
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Kingsbury, Gillian A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; TITLE OF INVENTION: MIXED LYMPHOCYTE LIBRARY
; FILE REFERENCE: MLN98-40PA
; CURRENT APPLICATION NUMBER: US/09/396,970
; CURRENT FILING DATE: 1999-09-14
; EARLIER APPLICATION NUMBER: 60/100,293
; EARLIER FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 8756
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 7559
; LENGTH: 4668
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4668)
; OTHER INFORMATION: n = A,T,C or G
US-09-396-970-7559
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## Alignment Scores:

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Pred. No.: 0 Length: 4668
Score: 4983.00 Matches: 948
Percent Similarity: 99.48% Conservative: 0
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Best Local Similarity: 99.48% Mismatches: 1
Query Match: 99.99% Indels: 4
DB: 23 Gaps: 4

US-09-671-687A-3 (1-949) x US-09-396-970-7559 (1-4668)

QY 1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIle 20
DB 230 ATGAGTTTCAGGCTTATGGAGCCAAAGAAAAGTCACTTCACTCCCTACTTGGGAAGACGGATT 289

QY 21 PheTyrLeuLeuLeuGlnCysSerValThrAspLysGlnThrGlnLysLeuLys 40
DB 290 TTTTACTTCTCTTCAAGATGTCAGCGTTACAGACAAACAAACAAAGCTCCCTTAAA 349

QY 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
DB 350 GTACCGAAGGGAAGTATAGGACAGATATATCAAGATCGTTCTGTGGGCGATTCAAGATT 409

QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnProHisAla 80
DB 410 CCTTCTGCAAAAGGCAAGAAAATCAGATTGATTTGATTTAAAAATTTCTAGAGCAACCTCATGCA 469

QY 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99
DB 470 GTTCTCTTGTGTGATGAAAAGGATGTTGTAGAGATAAATGAAAAGTTTCACAGAGTTACTTT 529

QY 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
DB 530 TTGGCAATTACCAATTGTGAGGAGAGGTTACGCTTGTAAACACGAAACAGACTTAAGT 589

QY 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
DB 590 AAAGCCTCCAAATAGACGTGGGCTGTCTGTGAAAGTACAGCTGAGATCTGGGGAAGAA 649

QY 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
DB 650 AAAATTTCTGGAGTTGTACGCTTTCAGAGGACCCCTGTGTAGCAGAGAGGACAGTCTCCGGA 709

QY 160 IlePhePheGlyValGluLeuLeuGluGlyArgGlyGlnGlyPheThrAspGlyVal 179
DB 710 ATATTCTTTGAGTTGAATTCGTGNAAGAGTCTGTTCAAGGTTTCTACGACGGGGTG 769

QY 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
DB 770 TACCAAGGGAACACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTGTCATTGGAC 829

QY 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
DB 830 AAGCTAGAACTCATAGAAGATGATGACACTGCAATTGGAAAGTGATTACGACAGTCTCTGGG 889

QY 219 AspThrMetGlnValGluLeuProLeuGluIleAsnSerArgValSerLeuLysGly 238
DB 890 GACCAATATGCAAGTTCGAACCTTCTCCCTTTGAAATATACTCCAGAGTTTCTTTGAAGGTT 949

QY 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
DB 950 GGAGAAACATAGAAATCTGGAAACAGTTATATCTGTGATGTTTTCGACAGAAAGAACG 1009

QY 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
DB 1010 TTAGGATATTTTGTGGTGTGACATGATAACCTATTGGCAACTGGGATGGAGATTT 1069

QY 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
DB 1070 GATGGAGTGCAGCTTTGTAGTTTTCGCTGTGTGAAAGTACAAATTTCTATTGACATCAAT 1129

QY 298 AspIleIleProGluSerValThrGlnGluArgArgProProLysLeuAlaPheMetSer 317
DB 1130 GATATCATCCAGAGAGTGTGACGAGAAAGGAGGCTCCCAAACTTGCCTTTATGTGCA 1189

QY 318 ArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThr 337
DB 1190 AGAGGTGTGGGACAAAGGTTTCATCCAGTCAATAAACCAGGCTACAGATCTACC 1249
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; SEQ ID NO 5019
; LENGTH: 4668
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(4668)
; OTHER INFORMATION: n = A,T,C or G
US-09-397-424-5019

Alignment Scores:
Pred. No.: 0 Length: 4668
Score: 4983.00 Matches: 948
Percent Similarity: 99.48% Conservatives: 0
Best Local Similarity: 99.48% Mismatches: 1
Query Match: 98.99% Indels: 4
DB: 23 Gaps: 4

US-09-671-687A-3 (1-949) x US-09-397-424-5019 (1-4668)

Qy 1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIle 20
Db 230 ATGAGTTTCAGGCTTATGGAGCCCAAGAAAAGTCACTTCCCTACTCGGAAGAGCGGATT 289
Qy 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40
Db 290 TTTTACTTGTCTTCAAGAAATGCGCGTTACAGACAAACAAACACAAAGAGCTCCTTAAA 349
Qy 41 ValProIleGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db 350 GTACCAAGAGGAGATATAGACAGTATATTCAAGATCGTTCTGTGGGCAATTCAGGATT 409
Qy 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnGlnProHisAla 80
Db 410 CCTTCTGCAAAAGCAAGAAAATACAGATTGGATTAAAAATTTAGAGCAACCTCATGCA 469
Qy 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99
Db 470 GTTCTCTTTGTTGATGAAAAGGATGTTGTAGAGATAAATGAAAAGTTTCACAGAGTTACTT 529
Qy 100 LeuAlaIleThrAsnCysGluLysArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db 530 TTGGCAATTTACCAATTTGTGAGGAGAGGTTTCAGGCTGTTTAAAAACAGAAACAGACTAAGT 589
Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
Db 590 AAGGCTCCAAATAGACGTGGGCTGTCCTGTGAAAGTACAGCTGAGATCTGGGGAAGAA 649
Qy 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
Db 650 AATTTTCTGGAGTTGTACGCTTCAGAGGACCCCTGTTAGCAGAGAGGACAGTCTCCGA 709
Qy 160 IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal 179
Db 710 ATATTCTTTGGAGTTGAATTTGCTGGAAGAAGGTCGTGGTCAAGGTTTCACTGACGGGGTG 769
Qy 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db 770 TACCAAGGGAACACAGCTTTTTCAGTGTGATGAAGATTGTGGCGGTGTTTGTTCATTGGAC 829
Qy 199 LysLeuLeuLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
Db 830 AAGCTAGAACTCATAGAGATGATGACATGCAATTTGGAAGATGATTACGCAAGGTCCTGGG 889
Qy 219 AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly 238
Db 890 GACACAATGCGAGTCGAATCTCTCTCTTGGAAATAAATCCAGAGTTCTTTTGAAGGTT 949
Qy 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db 950 GGAGAAACAATAAGATCTGGAACAGATTATTTCTGTGATGTTTTCAGGCAAGAAAGAGC 1009
Qy 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
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Db 1010 TTAGGATATTTTGTGGTGTGGACATGGATAACCTATTGGCACTGGGATGGAAGATT 1069
Qy 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
Db 1070 GATGGAGTGCAGCTTTGTAGTTTTCGCTGTCTGGAAGTACAAATCTATTGACATCAAT 1129
Qy 298 AspIleIleProGluSerValThrGlnGluArgArgProProLysLeuAlaPheMetSer 317
Db 1130 GATATCATCCAGAGAGTGTGACGAGAAAGGAGGCTCCCAAACTTGCCTTATGTCA 1189
Qy 318 ArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThrClySerThr 337
Db 1190 AGAGGTGTGGGCAAAAGGTTCTATCCAGTCAATAATAAACCAAGGCTACAGAGTCTACC 1249
Qy 338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356
Db 1250 TCAGACCTCGGAATAGAACAGATCTGAATATTTTATATACCTTAATGGGTCTTCTGT 1309
Qy 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376
Db 1310 GACTCACACCAACCAATCCAAATCAAAAATACATGGTACATTGATGAAGTTGCAGAAGAC 1369
Qy 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln 396
Db 1370 CCTGCAAAATCTCTTACAGAGATATCTACAGACTTTTGACCGTTCTTCCACCACTCCAG 1429
Qy 397 ProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416
Db 1430 CCTCCTCTGTGAACCTCACTGACCACCGAGAACAGATTCCACTCTTTTACCATTTCAGTCTC 1489
Qy 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436
Db 1490 ACCAAGATGCCAATACCAATGGAAGTATTGGCCACAGTCCACTTCTCTGTGAGCCGAG 1549
Qy 437 SerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro 456
Db 1550 TCTGTAATGGAAGAGCTAAACACTGCACCCGTCGAAGAGAGTCCACCTTGGCCATGCGCT 1609
Qy 457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476
Db 1610 CCTGGGAACCTCACATGTTGTAGAAAGTGGGCTCATTTGGCTGAAGTTAAGGAGAACCTCT 1669
Qy 477 PheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496
Db 1670 TTCTATGGGTATCCGTTGGATCGGTGAGCCACCAAGAGTGAATGAAGTGTCTGCTGGA 1729
Qy 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516
Db 1730 CTGGAACTGGAAGATGAGTGTGACGGCTGTACGGATGGAACCTTCAGAGGCACTCGGTAT 1789
Qy 517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLysSerCysArgProAspSer 536
Db 1790 TTCACCTGTGCTGGAAGAGGCGCTGTTGTGAAACTGGAAGAGCTGAGGCGCTGACTCT 1849
Qy 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556
Db 1850 AGGTTTCATTCATTCAGGCGGTTTCCAAATCAGATTGAGCGCTGTAACCTTTAGCATTT 1909
Qy 557 GlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGly 576
Db 1910 GGAGGCTACTTAAGTAGTAGTAGAAGAAATACTCCACCAAAAATCGAAAAAGAGGC 1969
Qy 577 LeuGluIleMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596
Db 1970 TTGGAGATAATGATTGGAAAGAGAGGAGGATCCAGGCTCATTAACAATCTTGTGTACTTA 2029
Qy 597 AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg 616
Db 2030 GACTCAACCTTATTCCTCTTATTTGCTTTAGTTTCTGTCTGGACACTGTGTACTTAGA 2089
Qy 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636
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Db 2090 CCCAAGAAAGACGATGTAGATATATATAGTGAACCCAGAGCTACTGAGACAGAA 2149
Qy 637 lIeValAenProLeuArglleTyrGlyTyrValCysAlaThrLyslleMetLysLeuArg 656
Db 2150 ATTGTTAATCTCTGAGAATATATGGATATGTGTGTCACAAATAATATGAAACTGAGG 2209
Qy 657 LyslleLeuGluLysValGluAlaSerGlyPheThrSerGluGluLysAspProGlu 676
Db 2210 AAAATACTTGAAAGGTTGGAGCTGTCATCAGGATTTACCTCTGAAGAAAAGATCCTGAG 2269
Qy 677 GluPheLeuAsnIleLeuPheHisIleuArgValGluProLeuLyslleArg 696
Db 2270 GAATTCITGAATATCTGTTTCATCATATTTAAGGGTAGAACCTTTGCTAAATAATAGA 2329
Qy 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716
Db 2330 TCAGCAGGTCAAAGGTACAAGATTGTTACTTCTATCAATTTTATGGAATAAATGAG 2389
Qy 717 LysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeu 736
Db 2390 AAAGTGGCGTTCACAAATTCAGCAGTTGTTAGATGGTCTTTTATCAACAGTAACCTG 2449
Qy 737 LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPhe 756
Db 2450 AAAATTCGAGGAGCACCATCATGCTGATTTATTCAGATGCCCTCGATTTGGAAGACATTT 2509
Qy 757 LysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuGluAsp 776
Db 2510 AAATATTTTAAAAAATTTTCTCTCTGGAATTAATATTAACAGATTTACTTTGAGAC 2569
Qy 777 ThrProArgGlnCysArglleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr 796
Db 2570 ACTCCAGACAGTCCCGGATATGAGGGCTTCGAATGTATGATGTAGAGATGCTAC 2629
Qy 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln 816
Db 2630 GAGCATCCGAGCATCTCAGCTGGAAAAATCAAGCAGTTTGTAAAAACCTGCAACACTCAA 2689
Qy 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrRhanProValSerLeuProLysAsp 836
Db 2690 GTCCACCTTCATCCGAAGAGCTGAATCATATAATATAACCCAGTGTCACTTCCCAAGAC 2749
Qy 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856
Db 2750 TTACCCGACTGGAGTGGAGACACGGCTGCATCCCTTCGACAGATATGGAGTTATTTGCT 2809
Qy 857 ValLeuCyslleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876
Db 2810 GTTCTCTGCATAGAAACAAGCCACTATGTTGCTTTTGTGAAGTATGGAAGGACGATTTCT 2869
Qy 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlnAsnGlyPheAsnIle 896
Db 2870 GCCTGGCTCTCTTTGTACAGCATGCGCGATCGGATGCTGATGAGATGGCTTCAACATT 2929
Qy 897 ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu 916
Db 2930 CCTCAAGTACCCCATCCCAAGATGAGAGATGACTTGAAGATGCTCTCTGGAAGACCTG 2989
Qy 917 HisSerLeuAspSerArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936
Db 2990 CATTCCTTGACTCCAGGAGATCCAGGCTGTGCAGGAGACTGCTTTGTGATGATAT 3049
Qy 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3050 ATGTGTCATGACAGAGTCCAAACATGAGTTTGTACAAA 3088
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## RESULT 10

US-09-397-424A-5019

; Sequence 5019, Application US/09397424A

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Pan, Yang

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A

; TITLE OF INVENTION: HUMAN OSTEOBLAST LIBRARY

; FILE REFERENCE: MLN98-45PM

; CURRENT APPLICATION NUMBER: US/09/397.424A

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,469

; PRIOR FILING DATE: 1998-09-15

; PRIOR APPLICATION NUMBER: 60/106,454

; PRIOR FILING DATE: 1998-10-30

; PRIOR APPLICATION NUMBER: 60/107,252

; PRIOR FILING DATE: 1998-11-05

; PRIOR APPLICATION NUMBER: 60/132,100

; PRIOR FILING DATE: 1999-04-30

; NUMBER OF SEQ ID NOS: 5379

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 5019

; LENGTH: 4668

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1) .. (4668)

; OTHER INFORMATION: n = A, T, C or G

US-09-397-424A-5019

## Alignment Scores:

Pred. No.:	0	Length:	4668
Score:	4983.00	Matches:	948
Percent Similarity:	99.48%	Conservative:	0
Best Local Similarity:	99.48%	Mismatches:	1
Query Match:	98.99%	Indels:	4
DB:	23	Gaps:	4

US-09-671-687A-3 (1-949) x US-09-397-424A-5019 (1-4668)

Qy 1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArglle 20

Db 230 ATGAGTTTCAGGCTTATGAGCCAAAGAAAGTCACTTCACCCCTACTGGGAAGAGCGGATT 289

Qy 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40

Db 290 TTTTACTTGTCTTCTCAAGAAATGACGCTTACAGCAACAAACAAACAAAGCTCTCTAAA 349

Qy 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArglle 60

Db 350 GTACCGAAGGAAGTATAGACAGTATATTCAAGATCGTCTGTGGGCGATTCAGGATT 409

Qy 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLyslleLeuGluGlnProHisAla 80

Db 410 CTTTCTGCAAAAGGCAAGAAATCAGATTGGATTTAAAAATTTCTAGAGCAACCTCATGCA 469

Qy 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99

Db 470 GTTCTCTTTGTGTATGAAAGGATGTTGTAGAGATAAATGAAAGTTTCAAGATTACTT 529

Qy 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119

Db 530 TTGCAATTTACCAATTTGTGAGAGAGGTTTACGCTGTTTAAAAACAGAAACAGACTAAGT 589

Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139

Db 590 AAAGGCTCCAAATAGACGTGGCTGTCTCTGTGAAGTACAGCTGAGATCTGGGAAGAA 649

Qy 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159

Db 650 AAATTTCTGAGTTGTACGCTTTCAGAGACCCCTGTTTAGCAGAGAGGACAGCTCTCCGGA 709

Qy 160 IlePhePheGlyValGluLeuLeuGluGlyArgGlyGlnGlyPheThrAspGlyVal 179

Db 710 ATATTTCTTTGGAGTTGAATTTCTGGAAGAGTCTGGTCAAGGTTTCTACGCGGGTG 769

Qy 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198

Db 770 TACCAAGGAAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTGTTGTCATTGGAC 829





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Db 2990 CATTCCTTGAGCTCCAGGAGAAATCCAAAGGCTGTGCACGAAAGACTGCTTTGTGATGCATAT 3049
QY 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3050 ATGTGCATGTACCAGAGTCCAAACAATGAGTTGTACAAA 3088
RESULT 11
US-09-432-241A-3760
; Sequence 3760, Application US/09432241A
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; TITLE OF INVENTION: HUMAN EPIDERMAL KERATINOCYTE LIBRARY
; FILE REFERENCE: 1600.1004001
; CURRENT APPLICATION NUMBER: US/09/432,241A
; CURRENT FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/106,445
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/107,227
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/127,182
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 60/132,099
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5041
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3760
; LENGTH: 4668
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(4668)
; OTHER INFORMATION: n = A, T, C or G
US-09-432-241A-3760
Alignment Scores:
Pred. No.: 0 Length: 4668
Score: 4983.00 Matches: 948
Percent Similarity: 99.48% Conservative: 0
Best Local Similarity: 99.48% Mismatches: 1
Query Match: 98.99% Indels: 4
DB: 24 Gaps: 4
US-09-671-687A-3 (1-949) x US-09-432-241A-3760 (1-4668)
QY 1 MetSerSerGlyLeuTyrSerGlnGluLysValThrSerProTyrTrpGluGluArgIle 20
Db 230 ATGAGTTTCAGGCTTATGGAGCCAAAGAAAGTCACTTCACCTACTGGGAGAGCGGATT 289
QY 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40
Db 290 TTTTACTTCTCTTCAAGATGACGCTTACAGACAAACACAAAGCTCTCTTAA 349
QY 41 ValProLysGlySerIleGlnTyrIleClnAspArgSerValGlyHisSerArgIle 60
Db 350 GTACCGAAGGGAAGTATAGGACAGATATATTCAGATCGTTCTGTGGGCGCATTCAGGATT 409
QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnProHisAla 80
Db 410 CCTTCTGCAAAAGGCAAGAAATACAGATGGGATTTAAATAATTCAGAGCAACCTCATGCA 469
QY 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99
Db 470 GTTCTCTTGTGATGAAAGAGATGTTGTAGAGTAAATGAAAGTTACAGAGTTACTT 529
QY 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db 530 TTGGCAATTACCAATTGTGAGGAGAGTTTCAGCCTGTTTAAATAACAGAAACAGACTAAGT 589
QY 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
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Db 590 AAAGGCTCCAAAATAGACGTGGGCTGCTCTGTGAAAAGTACAGCTGAGATCTGGGGAAGAA 649
QY 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
Db 650 AAATTTCTCGAGTTGTACGCTTCAGAGGACCCCTGTTAGCAGAGAGGACAGATCTCCGGA 709
QY 160 IlePhePheGlyValGluLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal 179
Db 710 ATATCTTTGGAGTTGAATTTGCTGGAAGAAGTCTGTGTCAAGGTTTCACTACCGGGTG 769
QY 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db 770 TACCAAGGGAACACAGCTTTTTCAGTGTGATGATGAGATTGTGGCGTGTGTTGTGTCATTGGAC 829
QY 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
Db 830 AAGCTAGAACTCATAGAAGATGATGACACTCATTTGGAAGTGTATTCAGCAGGTCTCTGG 889
QY 219 AspThrMetGlnValGluLeuProLeuGluIleAsnSerArgValSerLeuLysGly 238
Db 890 GACAAATGCAAGTTCGAACCTTCTCTTTGGAATAAACTCCAGAGTTCTTTGAAGGTT 949
QY 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db 950 GGAGAAACAATAGAAATCTGGAACTATATTTCTGTGATGTTTGGCCAGGAAAGAAAGC 1009
QY 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
Db 1010 TTAGGATATTTTGTGTGTGGCATGATGATACCTATTGGCAACTGGGATGGAAGATTT 1069
QY 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
Db 1070 GATGAGTGCAGCTTTGTAGTTTTCGCGTGTGTGAAAGTACAAATTCATTTGACATCAAT 1129
QY 298 AspIleIleProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSer 317
Db 1130 GATATCATCCAGAGAGTGTGACGAGGAAGAGGAGGCTCCCAAACTTGCCTTTATGTCA 1189
QY 318 ArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThr 337
Db 1190 AGAGGTGTGGGGACAAAGGTTTCATCCAGTCAATAAAACAAAGGCTACAGGATCTACC 1249
QY 338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356
Db 1250 TCAGACCTCGAAATAGAAACAGATCTGAATTTATATACCTTAAATGGGTCCTCTGT 1309
QY 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376
Db 1310 GACTCACACACACANTCAAAATCAAAAATACATGTTACATGTAAGATTGCAGAGAC 1369
QY 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProLeuGln 396
Db 1370 CCTGCAAAATCTCTTACAGAGATATTCAGACTTTCACCGTTCCTTACCACCATCCAG 1429
QY 397 ProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416
Db 1430 CCTCCTCTGTGAATCACTGACCAACAGAGATTCACCTCTTTTACCATTCAGTCTC 1489
QY 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436
Db 1490 ACCAAGATGCCCAATACAAATGGAAGTATTGGCCACAGTCCACTTCTCTGTGCCCCAG 1549
QY 437 SerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro 456
Db 1550 TCTGTATGGAAGAGCTAAACACTGCACCGCTCCAGAGAGATCCACCTTGGCCATGCT 1609
QY 457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476
Db 1610 CCTGGGAACACTCACATGCTAGAAAGTGGGCTCATTTGGCTGAAGTTAAGGAGAACCTCT 1669
QY 477 PheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496
```

Db 1670 TTCTATGGGGTAATCCGTTGGATCGGTCAGCCACCAGGACTGAATGAAGTGGCTCGCTGGA 1729  
QY 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516  
Db 1730 CTGGAACCTGGAAGATGAGTGTGAGGCTGTACGGATGGAACCTTCAGAGGCACTCGGTAT 1789  
QY 517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLysSerCysArgProAspSer 536  
Db 1790 TTCACTGTGCCCTGAAGAGGCGCTGTGTGTAAGCTGAAGAGCTGACGCGCTGACTCT 1849  
QY 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556  
Db 1850 AGGTTTGCACTATGTCAGCGGTTTCCATCAGATTGAGCGCTGTAACTCTTTAGCAATT 1909  
QY 557 GlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGly 576  
Db 1910 GGAGGCTACTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAAAAAGAGGC 1969  
QY 577 LeuGluIleMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596  
Db 1970 TTGGAGATAATGATGGGAAGAAAGGCAATCCAGGGTCATTACAAATTCCTTGTTACTTA 2029  
QY 597 AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg 616  
Db 2030 GACTCAACCTTATCTGCTTATTTGCTTTTGTGTTCTGTCGACACTGTGTTACTTAGA 2089  
QY 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636  
Db 2090 CCCAAAGAAAAGAACGATGAGAAATATATAGTGAACCCCAAGACTACTGAGACAGAA 2149  
QY 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656  
Db 2150 ATTGTTAATCCTCGAAGATATATGATATGTGTGCCACAAAAATTTATGAACCTGAGG 2209  
QY 657 LysIleLeuGluLysValGluAlaAlaSerGlyPheThrSerGluLysAspProGlu 676  
Db 2210 AAAATACTTTGAAAAGGTGAGGCTGCATCAGGATTTACCTCTCAAGAAAAAGATCCTGAG 2269  
QY 677 GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLysIleArg 696  
Db 2270 GAATCTTGAAATATCTGTTTCATCATATTTTAAAGGGTAGAAGCTTTGCTAAAAATAAGA 2329  
QY 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716  
Db 2330 TCAGCAGGTCAAAAGGTACAAGATTGTTACTTCTATCAAAATTTTATGGAATAAATGAG 2389  
QY 717 LysValGlyValProThrIleGlnGlnLeuLeuGluTyrSerPheIleAsnSerAsnLeu 736  
Db 2390 AAAAGTTGGCGTTCCCAAAATTCAGCAGTTGTTAGAATGGTCTTTTATCAACAGTAACCTG 2449  
QY 737 LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPhe 756  
Db 2450 AAAATTTGAGAGGCACCATCATGCTGTGATTAATTCAGATGCTCGATTTGGAAGAAGACTTT 2509  
QY 757 LysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAsp 776  
Db 2510 AAACATATTAAAAAAATTTTCTCTCTGGAATTAATAATAACAGATTTACTTTGAAGAC 2569  
QY 777 ThrProArgGlnCysArgIleCysGlyLeuAlaMetTyrGluCysArgGluCysTyr 796  
Db 2570 ACTCCAGACAGTCGCGGATATGTGAGGCGCTTGCAATGTATGAGTGTAGAGAATGCTAC 2629  
QY 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln 816  
Db 2630 GACGATCCGGACATCTCAGCTGGAAAAATCAAGCAGTTTTTGTAAAAACCTGCAACACTCAA 2689  
QY 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836  
Db 2690 GTCCACCTTCATCCGAAGAGGCTGAATCATATAATAAACCCAGTGTCACTTCCCAAGAC 2749  
QY 837 LeuProAspTyrAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856  
Db 2750 TTACCCGACTGGGACTGGAGACAGCGCTGCATCCCTTGGCAGAAATATGAGGTTATTGTCT 2809

QY 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876  
Db 2810 GTTCTCTGCATAGAAACAAGCCACTATGTTGCTTTTGTGAAGTATGGGAAGCAGCATCT 2869  
QY 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896  
Db 2870 GCCTGGCTCTTCTTTGACGATGGCGGATCGGATGGTGTGATGGCTTTCAACATT 2929  
QY 897 ProGlnValThrProCysProGluValGlyLysTyrLeuLysMetSerLeuGluAspLeu 916  
Db 2930 CCTCAAGTCAACCCCATGCCAGAGTAGGAGAGTACTTTGAAGATGTCTCTGGAAGACCTG 2989  
QY 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgLeuLeuCysAspAlaTyr 936  
Db 2990 CATTCCTTGGACTCCAGGAAATCCAAGGCTGTGCAGGAAGACTGCTTTGTGATGCATAT 3049  
QY 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949  
Db 3050 ATGTGCATGTACCAGATGCCAACAAATGAGTTGTACAAA 3088  
RESULT 12  
US-09-434-737-1278  
; Sequence 1278, Application US/09434737  
; GENERAL INFORMATION:  
; APPLICANT: Gearing, David P.  
; APPLICANT: Kingsbury, Gillian A.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A  
; TITLE OF INVENTION: HUMAN MIXED LYMPHOCYTE LIBRARY  
; FILE REFERENCE: 1600.1067001  
; CURRENT APPLICATION NUMBER: US/09/434, 737  
; CURRENT FILING DATE: 1999-11-05  
; EARLIER APPLICATION NUMBER: 60/107,228  
; EARLIER FILING DATE: 1998-11-05  
; NUMBER OF SEQ ID NOS: 1830  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1278  
; LENGTH: 4668  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(4668)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-434-737-1278

Alignment Scores:  
Pred. No.: 0 Length: 4668  
Score: 4983.00 Matches: 948  
Percent Similarity: 99.48% Conservative: 0  
Best Local Similarity: 99.48% Mismatches: 1  
Query Match: 98.99% Indels: 4  
DB: 24 Gaps: 4

US-09-671-687A-3. (1-949) x US-09-434-737-1278 (1-4668)

QY 1 MetSerSerCysLeuTrpSerGlnGluLysValThrSerProTyrTrpGluArgIle 20  
Db 230 ATGAGTTGAGGCTTATGGAGCCCAAGAAAAAGTCACTCCCTACTGGGAAGCGGATT 289  
QY 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40  
Db 290 TTTTACTTGTCTTCTTCAAGNATGCGGCTTACAGACAAACAAACAAAGCTCTTAAA 349  
QY 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60  
Db 350 GTACCAGAGGGAAGTAGTAGCAGATATATTCAAGATCGTTCTGTGGGCGATTCAAGGATT 409  
QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnProHisAla 80  
Db 410 CCTTCTGCAAAAGGCAAGAAAAATCAGATTGGATTAAAAATTTAGAGCAACCTCATGCA 469  
QY 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99

Db 470 GTTCTCTTCTTGATGATAAAGGATGTTGTAGAGATAAATGAAAAGTTTCACAGAGTTACTT 529  
Qy 100 LeuAlaIleThrAsnCysGluGluAArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119  
Db 530 TTGGCAATTAACCAATGTGTAGGAGAGGTTTTCAGGCTGTTTAAAAACAGAAAACAGACTAAGT 589  
Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139  
Db 590 AAAGGCTCCAAATAGACGTGGGCTGCTCTGTGNAAGTACAGCTGAGATCTGGGGAAGAA 649  
Qy 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159  
Db 650 AAATTTCTCGAGTTGTACGCTTCAGAGGACCCCTGTTAGCAGAGAGGACAGTCTCCGGA 709  
Qy 160 IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal 179  
Db 710 ATATTTCTTGGAGTTGAAATTTGCTGGAAAGAGGTGCTGGTCAAGGTTTTCACGTGCGGGGT 769  
Qy 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198  
Db 770 TACCAAGGAAACAGCTTTTTCAGTGTGATGAGATTGTGGGTGTTTGTTCGATTGGAC 829  
Qy 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218  
Db 830 AAGCTAGAACTCATAGAAGATGATGACACTGCATTGGAAAGTGATTACGCAGGTCCTGGG 889  
Qy 219 AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly 238  
Db 890 GACACAAATGAGGTGCAACTTCTCTTGGAAATAAATCCAGAGTTTCTTTGAAGGTT 949  
Qy 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258  
Db 950 GGAAACAAATAGAACTCGAAACAGTTATATTTCTGTGATGTTTTCAGGAAAGAAAGC 1009  
Qy 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278  
Db 1010 TTAGGATATTTTGTGTGTGGACATGATGATAACCTATTGGCAACTGGGATGGAAGATT 1069  
Qy 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297  
Db 1070 GATGGAGTGAGCTTTGTAGTTTTCGTGTGTTGAAAGTCAATTTCTATTGCAATCAAT 1129  
Qy 298 AspIleLeuProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSer 317  
Db 1130 GATATCATCCAGAGTGTGACGAGAAAGAGGCTCCCAAACTTGCCCTTATGTCA 1189  
Qy 318 ArgGlyValGlyAspLysGlySerSerSerHisAsnLysProLysAlaThrGlySerThr 337  
Db 1190 AGAGGTGTTGGGACAAAGGTTTATCCAGTCAATATTAACCAAGGCTACAGGATCTACC 1249  
Qy 338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356  
Db 1250 TCAGACCTGGAAATAGAAAACAGATCTGAATTTATTTATACCTTAAATGGGTCTTCTGTT 1309  
Qy 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376  
Db 1310 GACTCAACCAACCAATCAAAATCAAAATACATGATGATGATGATGATGATGATGATGATGAT 1369  
Qy 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln 396  
Db 1370 CCTGCAAAATCTCTTACAGAGATATCTACAGACTTTGACCGCTTCTTACCCACCACTCCAG 1429  
Qy 397 ProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu 416  
Db 1430 CCTCTCTCTGTGAATCTCACTGACCCAGACAGAGATTTCCACTCTTTTACCATTCAGTCTC 1489  
Qy 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436  
Db 1490 ACCAAGATGCCCAATACCAATGGAAGTATTTGGCCACAGTCTCTCTCTGTCTGAGCCGAG 1549  
Qy 437 SerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetPro 456

Db 1550 TCTTAATGGAAGAGCTAAACACACTGCACCCCTCCAGAGAGTCCACCCCTTGCCCATGCT 1609  
Qy 457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476  
Db 1610 CCTGGGAACATCACATGCTTAGAAGTGGGCTCATTTGGCTGAAGTTAAGGAGAACCTCTCT 1669  
Qy 477 PheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496  
Db 1670 TTCTATGGGGTAAATCCGTTGGATCGGTGAGCACCAGGACTGAATGAAGTCTCGCTGGA 1729  
Qy 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516  
Db 1730 CTGAACTGGAAGATGAGTGTGCAAGCTGTACGGATGGAACCTTCAGAGGCACTCGGTAT 1789  
Qy 517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLysSerCysArgProAspSer 536  
Db 1790 TTCACCTGTGCCCTGAAAGAGGCTGTTGTGAAACTGAAAGAGCTGCAGGCTGACTCT 1849  
Qy 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556  
Db 1850 AGTTTGCATCATTTGACCGCTTTCCAATCAGATTGAGCGCTGTAACTCTTTAGCATTT 1909  
Qy 557 GlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGly 576  
Db 1910 GGAGGCTACTTAACTGAAGTAGTAGAAGAAAATACTCCACCAAAAATGGAAGAGAGC 1969  
Qy 577 LeuGluIleMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596  
Db 1970 TTGGAGATAATGATTGGGAAAGAAAGGATCCAGGCTCATTAACAATTTCTTTACTTA 2029  
Qy 597 AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg 616  
Db 2030 GACTCAACCTTATCTCTCTTATTTGCTTTAGTTCTGTCTGGACACTGTGTACTTAA 2089  
Qy 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636  
Db 2090 CCCAAAGAAAGAACGATGTAGATAATATAGTCAAAACCCCAAGAGCTACTGAGGACAGAA 2149  
Qy 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656  
Db 2150 ATTGTTAATCTCTGAGAATATATGATGTGTGTGTCACAAATAATATGAACTGAGG 2209  
Qy 657 LysIleLeuGluLysValGluAlaAspGlyPheThrSerGluGluLysAspProGlu 676  
Db 2210 AAAATCTTGAAGAGGTGGAGCTGCATCAGATTATCTCTGAGAAAGAAAGATCCTGAG 2269  
Qy 677 GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLysIleArg 696  
Db 2270 GAATTTCTTGAATATTTCTGTTTCATCATATTTTAAAGGTAGAACCTTTGCTTAAATAAGA 2329  
Qy 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716  
Db 2330 TCAGCAGCTCAAAAGGTACAAAGATTGTTCTTCTTATCAAAATTTTATGGAAAAAATGAG 2389  
Qy 717 LysValGlyValProThrIleGlnGlnLeuLeuTrpSerPheIleAsnSerAsnLeu 736  
Db 2390 AAAGTTGGCGTGTCCCAAAATTCAGCAGTGTGTAGATGGTCTTTTATCAACAGTAACCTG 2449  
Qy 737 LysPheAlaGluAlaProSerCysLeuIleGlnMetProArgPheGlyLysAspPhe 756  
Db 2450 AAATTTGCAGAGGACCATCATGTCGATTTATTCAGATGCTCGATTTGGAAAAAGACTTT 2509  
Qy 757 LysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuAsp 776  
Db 2510 AAACATTTAAAAAAATTTTCTCTCTCTGAAATTAATAATAACAGATTTACTTGAAGAC 2569  
Qy 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGlyCysTyr 796  
Db 2570 ACTCCACAGACAGTCCGGATATGGAGGGCTTCAATGTATGATGTAGAGATGCTAC 2629  
Qy 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln 816  
Db 2630 GACGATCCGGACATCTCAGCTGGGAAATCAAGCAGTTTCTTAAACCTGCAACTCAA 2689

QY 817 ValHisLeuHisProLysArgLeuAenHisLysTyrAenProValSerLeuProLysAsp 836  
Db 2690 GTCCACCTTCATCCGAAGAGCTGAATCATAAATAAACCAGTGTCACTTCCCAAGAC 2749  
QY 837 LeuProAspTrpAspTrpArgHisGlyCysTleProCysGlnAenMetGluLeuPheAla 856  
Db 2750 TTACCCGACTGGGACTGGAGACCGCTGCATCCCTTGCAGAAATATGGAGTTATTGCT 2809  
QY 857 ValLeuCysTleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876  
Db 2810 GTTCTCTGCATAGAAACAAGCCACTATGTTGCTTTTGTGAAGTATGGAGGACGATCT 2869  
QY 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlnAenGlyPheAenIle 896  
Db 2870 GCCTGGCTCTCTTTGACAGCATGCCGATCGGATGGTGTGACAGATGGCTTCAACAT 2929  
QY 897 ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu 916  
Db 2930 CCTCAAGTCAACCATGCCAGAGATGAGGAGTGTGCAAGAGACTGCTTGTGATGCATAT 2989  
QY 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936  
Db 2990 CATTCCTTGACTCCAGAGATCCAAAGGCTGTGCAAGAGACTGCTTGTGATGCATAT 3049  
QY 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949  
Db 3050 ATGTGCATGTACCAAGTCCCAACATGAGTTGTACAAA 3088

## RESULT 13

US-09-850-118-1278  
; Sequence 1278, Application US/09850118  
; GENERAL INFORMATION:  
; APPLICANT: Gearing, David P.  
; APPLICANT: Kingsbury, Gillian A.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A  
; FILE REFERENCE: 1600.1067-002  
; CURRENT APPLICATION NUMBER: US/09/850.118  
; CURRENT FILING DATE: 2001-05-07  
; PRIOR APPLICATION NUMBER: US 60/107,228  
; PRIOR FILING DATE: 1998-11-05  
; PRIOR APPLICATION NUMBER: US 09/434,737  
; PRIOR FILING DATE: 1999-11-05  
; NUMBER OF SEQ ID NOS: 1830  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1278  
; LENGTH: 4668  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(4668)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-850-118-1278

Alignment Scores:  
Pred. No.: 0 Length: 4668  
Score: 4983.00 Matches: 948  
Percent Similarity: 99.48% Conservative: 0  
Best Local Similarity: 99.48% Mismatches: 1  
Query Match: 98.99% Indels: 4  
DB: 33 Gaps: 4

US-09-671-687A-3 (1-949) x US-09-850-118-1278 (1-4668)

QY 1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIle 20  
Db 230 ATGAGTTTCAGGCTTATGGAGCCCAAGAAAAAGTCACTTCAACCTACTGGGAAGACGGATT 289  
QY 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40  
Db 290 TTTTACTTGTCTTCTTCAAGATGACGGTTACAGACAAACAAACAAACAAACAAACCTCTTAA 349

QY 41 ValProLysGlySerIleGlyValNTrpIleGlnAspArgSerValGlyHisSerArgIle 60  
Db 350 GTACGAAGGGAAGTATAGGACAGTATATTCAAGATCGTTCTGTGGGCACTTCAAGAT 409  
QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80  
Db 410 CCTTCTGCAAAAGGCAGAAAAATCAGATTGGATTAAAAAATCTTAGAGCAACCTCATGCA 469  
QY 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99  
Db 470 GTTCTCTTTGTGATGAAAGAGTGTGTAGAGATAAATGAAGTTTACAGATTACTT 529  
QY 100 LeuAlaIleThrAenCysGluGluArgPheSerLeuPheLysAenArgAsnArgLeuSer 119  
Db 530 TTGGCAATTATCCAAATTGTGAGGAGAGGTTTACGCTGTTTAAAAACAGAAACAGACTAAGT 589  
QY 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuAenArgSerGlyGluGlu 139  
Db 590 AAAGGCTTCCAAATAGACGTGGCTGTCTGTGAAAGTACAGCTGAGATCTGGGGAAGAA 649  
QY 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159  
Db 650 AAATTTCTGAGTGTACGCTTACAGAGACCCCTGTAGCAGAGAGACAGTCTCCGGA 709  
QY 160 IlePhePheGlyValGluLeuLeuGluGluArgGlyArgGlyGlnGlyPheThrAspGlyVal 179  
Db 710 ATATTTCTGGAGTTGAATTCTGGAAGAGGTCGTGCTCAAGGTTTCTACTGACGGGTG 769  
QY 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198  
Db 770 TACCAAGGGAACAGCTTTTTCAGTGTGATCAAGATTCTGGCGTGTGTTGTTGTCATTGGAC 829  
QY 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218  
Db 830 AAGCTAGAACCTCATAGAAGATGATGACACTGCATTTGGAAGTGAATAGCAGAGTCTCGG 889  
QY 219 AspThrMetGlnValGluLeuProLeuGluLeuLeuAenSerArgValSerLeuLysGly 238  
Db 890 GACAAATGCAAGTGCAGAACTTCTCTTTGGAATAAATACTCCAGAGTTTCTTTGAAGTT 949  
QY 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258  
Db 950 GGAGAAACAATAGAAATCTGGAACAGTTATATCTGTGATGTTTTCAGGAGAAAGAAAGC 1009  
QY 259 LeuGlyTyrPheValGlyValAspMetAspAsnProLleGlyAsnTrpAspGlyArgPhe 278  
Db 1010 TTAGGATATTTTGTGTTGGTGGACATGATGAACCTATTGGCAACTGGGATGGAAGATTT 1069  
QY 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAen 297  
Db 1070 GATGGAGTGCAGCTTTTGTAGTTTTCGCTGTGTTGAAAGTACAATTTCTATTGACATCAAT 1129  
QY 298 AspIleIleProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSer 317  
Db 1130 GATATCATCCAGAGAGTGTGACGAGAAAGGAGGCTCCCAAACTTGCCTTTATGTCA 1189  
QY 318 ArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThr 337  
Db 1190 AGAGTGTGTGGGACAAAGGTTTCCAGTCATATAAACCAGGCTACAGGATCTACC 1249  
QY 338 SerAspProGlyAenArg---ArgSerGluLeuPheTyrThrLeuAenGlySerSerVal 356  
Db 1250 TCAGACCTCGAAATAGAAAACAGATCTGAATTTATTTATACCTTAAATGGGTCTTCTGT 1309  
QY 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376  
Db 1310 GACTCACAAACCAATCCAAATCAAAATAAATACATGGTACATTGATGAAGTTGCAAGAC 1369  
QY 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProLeuGln 396  
Db 1370 CCTGCAAAATCTCTTACAGAGATATCTACAGACTTTGACCGGTTCTTACACCACTCCAG 1429



Db 1585 ATGAGTTACGGCTTATGGAGCCCAAGAAAAGTCACTCACCTACTCGGAGAGCGGATT 1644  
Qy 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLys 40  
Db 1645 TTTTACTTGCTTCTTCAAGAATGAGGTTACAGACAAACAAACAGAAAGCTCTTAAA 1704  
Qy 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60  
Db 1705 GTACCGAAGGAAAGTAGTAGACAGTATATTAAGATCGTTCTGTGGGCGATTCAAGGATT 1764  
Qy 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnGlnProHisAla 80  
Db 1765 CCTTCGCAAAAGCGAAGAAAATCAGATTGGATTAAAAATTTAGAGCAACCTCATGCA 1824  
Qy 81 ValLeuPheValAspGlu---AspValValGluIleAsnGlnLysPheThrGluLeuLeu 99  
Db 1825 GTTCTCTTTGTCATGAAGAGGATGTTGTAGAGATAAATGAAAAGTTTACAGAGTTACTT 1884  
Qy 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119  
Db 1885 TTGGCAATTTACCAATTTGTGAGGAGAGGTTTCAGCGCTGTTTAAAAACAGAAACAGACTAAGT 1944  
Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139  
Db 1945 AAGGCGCTCCAAATAGACGTGGGCTGTCTGTGAAAGTACAGCTGAGATCTGGGGAAGAA 2004  
Qy 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159  
Db 2005 AATTTTCTGGAGTTGTACGCTTCAGAGGACCCCTGTTAGCAGAGGACAGTCTCCGGA 2064  
Qy 160 IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal 179  
Db 2065 ATATTCTTTGGAGTTGAAATGCTGGAGAGGTCGTGCTCAAGGTTTCACTGACGGGGTG 2124  
Qy 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198  
Db 2125 TACCAAGGAAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTGTGCAATTGGAC 2184  
Qy 199 LysLeuLeuLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218  
Db 2185 AAGCTAGAACTCATAGAAGATGATGACCTGCAATGGAAAGTATTACGCGAGTCTCTGGG 2244  
Qy 219 AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly 238  
Db 2245 GACACATCGAGGTCGACTTCTCTCTTGGAAATAAATCCACAGATTCTTTGAAGGTT 2304  
Qy 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258  
Db 2305 GGAGAAACAAATAGAATCTGGAACAGTTATATCTGTGATGTTTTCAGGAAAGAAAGC 2364  
Qy 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278  
Db 2365 TTAGGATATTTGTTGGTGTGGACATGGGATAACCTATTGGCAACTGGGATGAAGATT 2424  
Qy 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297  
Db 2425 GATGGAGTCAGCTTTGTAGTTTGGCGTGTGTTGAAAGTACAATTCTATTGGACATCAAT 2484  
Qy 298 AspIleIleProGluSerValThrGlnGluArgArgProProLysLeuAlaPheMetSer 317  
Db 2485 GATATCATCCAGAGAGTGTGACGACGAGAAAGAGGCGCTCCCAAACTTGGCTTTATGTCA 2544  
Qy 318 ArgGlyValGlyAspLysGlySerSerHisAsnLysPheProLysAlaThrGlySerThr 337  
Db 2545 AGAGGTGTTGGGGAACAAAGGTTTCATCCAGTCATAATAAACCAAGGCTACAGGATCTACC 2604  
Qy 338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356  
Db 2605 TCAGAGCCCTGGAAATAGAAACAGATCTGAATATTTTATACCTTAAATGGGCTCTCTGTT 2664  
Qy 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376  
Db 2665 GACTCACACCAACCAATCCAAATCAAAAAATACATGGTATCATTTGATGAAGTTGCAGAGAC 2724

Qy 377 ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln 396  
Db 2725 CCTCAAAATCTCTTACAGAGATATCTACAGACTTTGACCGTCTTCCACCACCATCCAG 2784  
Qy 397 ProProProValAsnSerLeuThrGluAsnArgPheHisSerLeuProPheSerLeu 416  
Db 2785 CCTCCTCTGTGAACCTCACTGACCACCGAAGACAGATTCCACTCTTTTACCATTCAGTCTC 2844  
Qy 417 ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln 436  
Db 2845 ACCAAGATGCCAATATACCAATGGAAGTATTGGCCACAGTCCACTTCTCTGTGACGCCAG 2904  
Qy 437 SerValMetGluGluLeuAsnThrAlaProValGlnGlnSerProProLeuAlaMetPro 456  
Db 2905 TCTGTATGAGAGAGCTAAACACTGCACCCGTCGAAGAGAGTCCACCCCTTGGCCATGCT 2964  
Qy 457 ProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProPro 476  
Db 2965 CCTGGAACTCACATGCTTAGAAGTGGCTCATTTGGCTGAAGTTAAGGAGAACCTCTCT 3024  
Qy 477 PheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGly 496  
Db 3025 TTCTATGGGGTAATCCGTTGGATCGGTGAGCCACAGGACTGAATGAAGTGTCTCGTGA 3084  
Qy 497 LeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyr 516  
Db 3085 CTGGAATGGAAGATGAGTGTGAGGCTGTACGATGGAACCTTCAGAGGCACTCGGTAT 3144  
Qy 517 PheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSer 536  
Db 3145 TTCACCTGTCCCTGAAGAGGCGCTGTTGTGAACTGAAGAGCTGCAGGCTGACTCT 3204  
Qy 537 ArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPhe 556  
Db 3205 AGGTTTGCATCATTTGACGCGGTTTCCAATCAGATTGAGCGCTGTAACTCTTTTAGCATTT 3264  
Qy 557 GlyGlyTyrLeuSerGluValValGluAsnThrProProLysMetGluLysGluGly 576  
Db 3265 GGAAGGCTACTTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATCGAAAAAGAGGC 3324  
Qy 577 LeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeu 596  
Db 3325 TTGGAGATATGATTGGGAAGAGAAAGGCATCCAGGGTCAATTACAATCTTGTACTTA 3384  
Qy 597 AspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArg 616  
Db 3385 GACTCAACCTTATTCTGCTTATTGCTTTTAGTTTCTGTTCTGGACACTGTGTACTTGA 3444  
Qy 617 ProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGlu 636  
Db 3445 CCCAAAGAAAAGAACGATGTAGAATAATTATAGTGAACCCCAAGAGCTACTGAGGACAGA 3504  
Qy 637 IleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArg 656  
Db 3505 ATTGTTAATCCTCTGAGAATATATGGATATGTGTGTGCCAAAAATTTATGAACCTGAGG 3564  
Qy 657 LysIleLeuGluLysValGluAlaAlaSerGlyPheThrSerGluGluLysAspProGlu 676  
Db 3565 AAAATACTTGAAGGTGGAGGCTGCATCAGGATTTTACTCTGAAGAAAAAGATCTCTGAG 3624  
Qy 677 GluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArg 696  
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Qy 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716  
Db 3685 TCAGCAGGTCAAAGGTACAAAGATTGTTACTTCTATCAAAATTTTATGGAAAAAATGAG 3744  
Qy 717 LysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeu 736  
Db 3745 AAAGTTGGCGCTTCCCAATTCAGCAGTTGTAGATGGTCTTTTATCAACAGTAACCTG 3804









US-09-671-687A-3 (1-949) x US-10-170-235-39761 (1-6871)	
Qy	1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluArgIle 20
Db	278 ATGAGTTCAGGCTTATGAGCCAAAGAAAAGTCACCTTACCCCTACTGGGAAGACGGATT 337
Qy	21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLys 40
Db	338 TTTTACTTGGCTTCTTCAAGATGAGCGTTACAGACAAACAAACACAAAAGCTCTTTAAA 397
Qy	41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db	398 GTACCGAAGGAAGATAGGACAGTATATCAAGATCGTTCTGTGGGCGATTTCGAAGATT 457
Qy	61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80
Db	458 CCTTCTGCAAAAGGCAAGAAAATCAGATTGGATTAAAAATTTCTAGAGCAACCTCATGCA 517
Qy	81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99
Db	518 GTTCTCTTGTGTGATGAAAAGATGTTGTAGAGATAAATGAAAAAGTTTCACAGAGTTACTT 577
Qy	100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db	578 TTGGCAATATTACCAATGTGAGGAGAGGTTTCAGCTCTGTTAAAAACAGAAAACAGACTAAGT 637
Qy	120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
Db	638 AAGGCTCCANATAGACGTGGGCTGTCTGTGAAGTACAGCTGAGATCTGGGGAGAA 697
Qy	140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
Db	698 AAATTTCTCGAGTTGTACGCTTCAGAGGACCCCTGTTAGCAGAGAGGACAGCTCTCCGGA 757
Qy	160 IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal 179
Db	758 ATATTTCTTGGAGTTGAATTTCTCGAAGAAGTCTGCTGTAAGTTCACCTGACGGGGTG 817
Qy	180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db	818 TACCAGGGAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTGTTCATATGGAC 877
Qy	199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
Db	878 AAGCTGAAGACTCATAGAAGATGATGACACTGCATTGGAAAGTGATTACGCAGGTCCTGGG 937
Qy	219 AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly 238
Db	938 GACACAATGCAGGTCGAACTTCTCTTGGAAAATAAACTCCAGAGTTTCTTTGAAGTT 997
Qy	239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db	998 GGAGAAACAATAGAAATCTGGAACAGTTATATCTGTGATGTTTTCGACGAAAAAGNAAGC 1057
Qy	259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
Db	1058 TTAGGATATTTTGTGTGTGGACATGGATNAACCTATTGGCAACTGGGATGGGAAGATT 1117
Qy	279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
Db	1118 GATGGAGTGCAGCTTGTAGTTTGTGGTGTGTTGAAAGTACAAATCTATTGACATCAAT 1177
Qy	298 AspIleIleProGluSerValThrGlnGluArgArgProProLysLeuAlaPheMetSer 317
Db	1178 GATATCATCCAGAGATGTGACCGCAGAAAGGAGGCTCCCAAACTTGCCCTTTATGTGCA 1237
Qy	318 ArgGlyValGlyAspLysGlySerSerSerHisAsnLysProLysAlaThrGlySerThr 337
Db	1238 AGAGGTGTGGGGHCAAAAGTTTCATCCAGTCATTAATAACCAAGGCTACAGGATCTACC 1297
Qy	338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356

QY 717 LysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeu 736  
Db 2438 AAAGTTGGCGTTCCCAATTCAGCAGTTGTAGAAATGGCTTTTATCAACAGTAACCTG 2497  
QY 737 LysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPhe 756  
Db 2498 AAATTTGAGAGGACCATCATGTCTGATATTAGATGCTCGATTTGGAAGAAGCTTT 2557  
QY 757 LysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAsp 776  
Db 2558 AAACATTTTAAAAAATTTTCTCTCTGGAATTAATATATACAGATTTACTTGAAGAC 2617  
QY 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr 796  
Db 2618 ACTCCAGACAGTCCGCGATATGTGGAGGCTTGCAATGTATGATGATAGAGAATGCTAC 2677  
QY 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln 816  
Db 2678 GACGATCCGACATCTCAGCTGGAAATCAAGCAGTTTTGTAAACCTGCAACACTCAA 2737  
QY 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836  
Db 2738 GTCCACCTTCATCCGAAGAGCTGAATCATATATATTAACCCAGTGTCACTTCCCAAGAC 2797  
QY 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856  
Db 2798 TTACCCGACCTGGAGCTGGACACGCTGCATCCCTGGCAGAAATATGGAGTTATTGTCT 2857  
QY 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876  
Db 2858 GTTCTCTGATAGAAAACAGCCACTATGTGTCTTTGTGAAGTATGGGAAGGACGATTCT 2917  
QY 877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896  
Db 2918 GCTGTGCTCTTCTTGACAGCATGGCCGATCGGAGTGGTGGTGAATGGCTTCAACATT 2977  
QY 897 ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu 916  
Db 2978 CCTCAAGTCACCCCATGCCAGAGTAGGAGAGTACTTGAAGATGCTCTGGAAGACCTG 3037  
QY 917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAlaTyr 936  
Db 3038 CATTCCTTGACTCCAGGAGATCCAAAGCTGTGCAGAGACTGCTTTGTGATGCATAT 3097  
QY 937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949  
Db 3098 ATGTGATGTACAGAGTCCAAATGAGTTGTACAAA 3136

## RESULT 17

PCT-US02-14570-3  
; Sequence 3. Application PC/TUS0214570  
; GENERAL INFORMATION:  
; APPLICANT: IMMUNEX CORPORATION  
; APPLICANT: Derry, Jonathan M. J.  
; APPLICANT: Fanslow III, William  
; APPLICANT: Dougall, William C.  
; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING  
; FILE REFERENCE: 3198-WO  
; CURRENT APPLICATION NUMBER: PCT/US02/14570  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: 09/851,673  
; PRIOR FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 5371  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (392)..(3262)  
; OTHER INFORMATION:

## PCT-US02-14570-3

Alignment Scores:  
Pred. No.: 0 Length: 5371  
Score: 4971.50 Matches: 948  
Percent Similarity: 99.16% Conservative: 0  
Best Local Similarity: 99.16% Mismatches: 1  
Query Match: 98.76% Indels: 7  
DB: 1 Gaps: 5

US-09-671-687A-3 (1-949) x PCT-US02-14570-3 (1-5371)

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QY 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40  
Db 452 TTTTACTTGTCTTCTCAAGAAATGACGCGTTACAGACAAACAAACAAAGCTCTCTTAAA 511  
QY 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60  
Db 512 GTACCGAAGGAAAGTATAGACAGTATATTCAAGATCGTTCTGTGGGCAATTCAGGATT 571  
QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80  
Db 572 CTTTCTCAAAAGCAAGAAAATCAGATTGGATTAAAAATTTAGAGCAACCTCATGCA 631  
QY 81 ValLeuPheValAspGlu---AspValValGluLeuAsnGluLysPheThrGluLeuLeu 99  
Db 632 GTTCTCTTGTGATGAAAAGGATGTTGTAGAGATAAATGAAAAGTTTCAAGAGTTACTTT 691  
QY 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119  
Db 692 TTGSCAAATACCAATTTGTGAGGAGAGGTTACGCTGTTTAAAAACAGAAAACAGATAAGT 751  
QY 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139  
Db 752 AAAGGCTCCAAATAGACGTGGGCTGTCTGTGAAAGTACAGCTGAGATCTGGGGAAGAA 811  
QY 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159  
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QY 160 IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal 179  
Db 872 ATATCTTTGGAGTTGAATTTGCTGGAAGAGGTCGTGTCAGGTTTCACTGACGGGGTG 931  
QY 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198  
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QY 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218  
Db 992 AAGCTAGAACTCATAGAAGATGATGACACTGCAATTTGAAAAGTGTATACGAGGTCCTGG 1051  
QY 219 AspThrMetGlnValGluLeuProLeuGluLeuAsnSerArgValSerLeuLysGly 238  
Db 1052 GACACATGCGAGTTCGAATCTCTCTTTGGAATAAATCCAGAGTTTCTTTTGAAGTTT 1111  
QY 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258  
Db 1112 GGAGAAACAATAGAACTGGAACAGTTATATCTGTGATGTTTTCGCCAGGAAAAGAAAGC 1171  
QY 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278  
Db 1172 TTAGGATATTTGTGTTGGTGGACATGATAACCTTATGGCAACTGGAGTGAAGATT 1231  
QY 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297  
Db 1232 GATGGAGTGCAGCTTTTGTAGTTTTCGTTGTTGAAAGTACAATTTCTATTTCACATCAAT 1291  
QY 298 AspIleIlePro-----GluSerValThrGlnGluArgArgProProLysLeuAla 314



; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (392)..(3262)  
US-09-851-673-3

## Alignment Scores:

Pred. No.: 0 Length: 5371  
Score: 4971.50 Matches: 948  
Percent Similarity: 99.16% Conservativeness: 0  
Best Local Similarity: 99.16% Mismatches: 1  
Query Match: 98.76% Indels: 7  
DB: 33 Gaps: 5

US-09-671-687a-3 (1-949) x US-09-851-673-3 (1-5371)

QY 1 MetSerSerGlyLeuThrSerGlnGluValThrSerProTyrTrpGluGluArgIle 20  
DB 392 ATGAGTTTCAGGCTTATGGAGCCCAAGAAAAAGTCACTTCACCCCTACTGGGAAGAGCGGATT 451  
QY 21 PheTyrLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40  
DB 452 TTTTACTTGCTTCTTCAAGATGCGAGGTTACAGACAAACAAACAAAGCTCCTTAA 511  
QY 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60  
DB 512 GTACCGAAGGAGATGAGACAGTATATTCAAGATCGTTCTGTGGGCGATCAAGGATT 571  
QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80  
DB 572 CCTTCTGCAAAAGCAAGAAAAATCAGATTGGATTAAAAATTCATAGACCACTCATGCA 631  
QY 81 ValLeuPheValAspGlu---AspValValGluLeuAsnGluLysPheThrGluLeuLeu 99  
DB 632 GTTCTCTTTTGTATGAAAGGATGTTGTGAGAGATAAATGAAAGTTTCACAGAGTTACTT 691  
QY 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119  
DB 692 TTGGCAATTACCAATTGTGAGGAGAGGTTTCCCTCTGTTTAAACACAGAACAGACTAAGT 751  
QY 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139  
DB 752 AAAGGCTCCAAATAGACGTGGGCTGCTCTGTGAAAGTACAGCTGAGATCTGGGGAAGAA 811  
QY 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159  
DB 812 AAATTTCTCGAGTTGTACGCTTTCAGAGGACCCCTGTTAGCAGAGGACAGCTCCGGA 871  
QY 160 IlePhePheGlyValGluLeuLeuGluGluArgGlyGlnGlyPheThrAspGlyVal 179  
DB 872 ATATTCTTTGGAGTTGAAATGCTGGAAGAAGTCTGTGTAAGTTTCACTGACGGGGTG 931  
QY 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198  
DB 932 TACCAAGGGAACAGCTTTTTCAGTGTGATGAAGATTGTGCGGTGTTTGTTCATTGGAC 991  
QY 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218  
DB 992 AAGCTAGAACTCATAAGAATGATGACACTGCATTGGAAAGTGATTACCGCAGGTCCTGGG 1051  
QY 219 AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly 238  
DB 1052 GACACAAATGAGGTCGAACCTTCCTCTTGGAAATAAACTCCAGAGTTCTTTTGAAGGTT 1111  
QY 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258  
DB 1112 GGAGAAACAATAGAACTGGAACAGTTATATTCTGTGATGTTTCCAGGGAAGAAAGC 1171  
QY 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278  
DB 1172 TTAGGATATTGTTGGTGTGGACATGATAACCTTATGGCAACTGGGATGGAGGATT 1231

QY 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297  
DB 1232 GATGAGTGCAGCTTTGTAGTTTGTGAAAGTACAATTTCTATTGACATCAAT 1291  
QY 298 AspileIlePro-----GluSerValThrGlnGluArgProProLysLeuAla 314  
DB 1292 GATATCATCCAGCTTTATCAGAGAGTGTGCGCAGGAAAGAGGCTCCCAACTTGCC 1351  
QY 315 PheMetSerArgGlyValGlyAspLysGlySerSerSerHisAsnLysProLysAlaThr 334  
DB 1352 TTTATGTCAGAGGTTGTTGGGACAAAGTTTCATCCAGTCATAATAAACAAGGCTACA 1411  
QY 335 GlySerThrSerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGly 353  
DB 1412 CGATCTACCTCAGACCCCTGGAAATAGAAAACAGATCTGAATTTATTTATACCTTTAAATGGG 1471  
QY 354 SerSerValAspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluVal 373  
DB 1472 TCTTCTGTGTGACTCAACACCAATCCAAATCAAAATAATACATGGTACATGATGAAGTT 1531  
QY 374 AlaGluAspProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerPro 393  
DB 1532 GCAGAGACCTTCGCAAAATCTCTTACAGAGATATCTACAGACTTTGACCGTTCTTACCA 1591  
QY 394 ProLeuGlnProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuPro 413  
DB 1592 CCACTCCAGCCTCTCTCTGTGAACCTCACTGACCAACGAGAAACAGATTTCCACTCTTTACCA 1651  
QY 414 PheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeu 433  
DB 1652 TTCAGTCTCAACCAAGATGCCAATACCAATGGAAGTATTGGCCACAGTCCACTTTCTCTG 1711  
QY 434 SerAlaGlnSerValMetGluGluLeuAsnThrAlaProValGlnGluSerProProLeu 453  
DB 1712 TCAGCCCAAGTCTGTAATGGAAGAGCTAAACACTGCACCCGTCAGAGAGTCCACCCTTG 1771  
QY 454 AlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGlu 473  
DB 1772 GCCATGCCCTCTGGGAACCTACATGGTCTAGAAAGTGGGCTCATTTGGCTGAAGTAAAGGAG 1831  
QY 474 AsnProProPheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluVal 493  
DB 1832 AACCCCTCTTCTATGGGGTAAATCCGTTGGATCGGTTCAGCCACCCAGGACTGAATGAAGTG 1891  
QY 494 LeuAlaGlyLeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGly 513  
DB 1892 CTCGCTGAGACTGGAACTGGAAGATGAGTGTGAGGCTGTACGGATGGAAACCTTCAGAGGC 1951  
QY 514 ThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArg 533  
DB 1952 ACTCGGTATTTCACTGTCCTGAGAGGGGCTGTTTGTGAACCTGAAGAGCTGCAGG 2011  
QY 534 ProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSer 553  
DB 2012 CCTGACTAGTGTTCATCATTTGAGCCGGTTTCCAATCAGATTGAGCGCTGAATCTCT 2071  
QY 554 LeuAlaPheGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGlu 573  
DB 2072 TTAGCATTTGAGGCTACTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAA 2131  
QY 574 LysGluGlyLeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSer 593  
DB 2132 AAGAAGCTTTGGAGATTAATGTTGGGAAGAAAGAAAGGCATCCAGGCTCATTAACAATCT 2191  
QY 594 CysTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrVal 613  
DB 2192 TGTACTTAGACTCAACCTTATCTGCTTATTTGCTTTTAGTTCTGTTCTGGACACTGTG 2251  
QY 614 LeuLeuArgProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeu 633  
DB 2252 TTACTTAGACCAAAAGAAAGAACGATGTAGAATATTATAGTGAACCAACCAAGAGCTACTG 2311  
QY 634 ArgThrGluIleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMet 653

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Db 2312 AGGACAGAAATGTTAACTCTCAGAAATATATGATATGTTGTCACACAAAATATG 2371
Qy 654 LysLeuArgLysIleLeuGluLysValGluAlaLaserGlyPheThrSerGluGluLys 673
Db 2372 AAACAGGAAATACCTTGAAGGTGGAGCTGCATCAGGATTTACCTCTGAAGAAAA 2431
Qy 674 AspProGluGluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeu 693
Db 2432 GATCCTCAGGAATCTTGAATATCTGTTTCATCATATTTTAAGGGTAGAACCTTTGCTA 2491
Qy 694 LysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGlu 713
Db 2492 AAAATAAGATCAGCAGGTCAAAAGGTACAAGATTTGTTACTTCTATCAAAATTTTATGGA 2551
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Db 2552 AAAAATCAGAAAGTTGGCGTTCCCACAATTCAGCAGTTGTTAGAAATGGTCTTTTATCAAC 2611
Qy 734 SerAsnLeuLysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGly 753
Db 2612 AGTAACTGAAATTTGAGAGGCACCATCATGCTGTGATTTATTCAGATGCCCTCGATTTGGA 2671
Qy 754 LysAspPheLysLeuPheLysIlePheProSerLeuGluLeuAsnIleThrAspLeu 773
Db 2672 AAAGACTTTAAACTATTAAAAAATTTTCTCTCTGGAATTAATAATATAACAGATTTA 2731
Qy 774 LeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArg 793
Db 2732 CTTGAAGACATCTCCAGACAGTCGGGATATGTGGAGGGCTTGCAATGTATGAGTGTAGA 2791
Qy 794 GluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCys 813
Db 2792 GAATGCTACGACGATCCGACATCTCAGCTGGAAAAATCAAGCAGTTTTTGTAAAAACCTGC 2851
Qy 814 AsnThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeu 833
Db 2852 AACACTCAAGTCCACCTTCATCCGAGAGGCTGAATCATNAATATAACCCAGTGTCACTT 2911
Qy 834 ProLysAspLeuProAspTyrAspTyrPargHisGlyCysIleProCysGlnAsnMetGlu 853
Db 2912 CCCAAAGACTTACCCGACTGGGACTGGAGACACGGCTGCATCCCTTGCAGAAATATGGAG 2971
Qy 854 LeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLys 873
Db 2972 TTATTTGCTGTCTCTGCATAGAAACAAGCCCACTATGTTGCTTTGTGAAGTATGGGAAG 3031
Qy 874 AspAspSerAlaTyrLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGly 893
Db 3032 GACGATTTGCTGCTGCTCTTTTGACAGCATGGCCGATCGGATGGTGGTCAGNATGGC 3091
Qy 894 PheAsnIleProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeu 913
Db 3092 TTCAACATTTCTCAAGTCACCCATGCCAGAGTAGGAGAGTACTTCAAGATGCTCTG 3151
Qy 914 GluAspLeuHisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCys 933
Db 3152 GAAACCTGCAATTCCTTGACTCCAGGAGAAATCCAAAGCTGTGCACGAAGACTGCTGTTGT 3211
Qy 934 AspAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db 3212 GATGCATATATGTGCATGTACAGATCCAAATGAGTTTGTACAAA 3259
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## RESULT 19

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US-10-755-889-489
; Sequence 489, Application US/10755889
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
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; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 489
; LENGTH: 5371
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-489

Alignment Scores:
Pred. No.: 0 Length: 5371
Score: 4971.50 Matches: 948
Percent Similarity: 99.16% Conservative: 0
Best Local Similarity: 99.16% Mismatches: 1
Query Match: 98.76% Indels: 7
DB: 61 Gaps: 5

US-09-671-687A-3 (1-949) x US-10-755-889-489 (1-5371)

Qy 1 MetSerSerGlyLeuTyrSerGlnGluLysValThrSerProTyrTrpGluGluArgIle 20
Db 392 ATGAGTTTCAGGCTTATGGAGCCCAAGAAAAGTCACTTCACTTACCTTCTGGGAAGACGGATT 451
Qy 21 PheTyrLeuLeuGlnGluCysSerValThrAspLysGlnThrClnLysLeuLeuLys 40
Db 452 TTTTACTTGTCTTCTCAAGAAATGCAGCGTTACAGACAAAACAACAAAAGCTCCTTAAA 511
Qy 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db 512 GTACCGAAGGAGTATAGGACAGTATATTCAGATCGTCTGTGGGCATTTCAAGGATT 571
Qy 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80
Db 572 CTTCTCGAAAAGGCAAGAAAATCAGATTGATTGATTAATAAATTCAGAGCAACCTCATGCA 631
Qy 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99
Db 632 GTTCTCTTGTGTGATGAAGAGGATGTTGAGAGATAAATGAAGTTCAAGAGTTACTT 691
Qy 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db 692 TTGGCAATTTACCAATTTGAGGAGAGGTTTCACCTCTGTTTAAAACAGAACACAGCTAAGT 751
Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
Db 752 AAAGSCCTCCAAATAGACGTGGGCTGCTCTGTGAAGTACAGCTGAGATCTGGGGAAGAA 811
Qy 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
Db 812 AAATTTCTCGAGTGTACGCTTCAGAGACCCCTGTTTAGCAGAGAGGACAGCTCCCGA 871
Qy 160 IlePhePheGlyValGluLeuLeuGluGluArgGlyGlnGlyPheThrAspGlyVal 179
Db 872 ATATTCTTTGGAGTTGAATTTGCTGGAAGAGGTCGTGGTCAAGGTTTCTAGCAGGGGTG 931
Qy 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db 932 TACCAAGGGGAACACGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTGTTCATTGGAC 991
Qy 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218
Db 992 AAGCTAGAACTCATAGAAGATGATCAGCTGATGGAAGATTGGAAGTATACGACGCTCTGGG 1051
Qy 219 AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly 238
Db 1052 GACACAAATGCAGGTGAACTTCTCTCTTTGGAAATAAATCCAGAGTTTCTTTGAGGTT 1111
Qy 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db 1112 GGAGAAACAATAGAAATCTGGAACAGTTATATCTGTGATGTTTGTCCAGGAAAAGAACG 1171
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; APPLICANT: Fanslow, William  
 ; APPLICANT: Dougall, William  
 ; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING  
 ; FILE REFERENCE: 3198  
 ; CURRENT APPLICATION NUMBER: US/10/760,678  
 ; CURRENT FILING DATE: 2004-01-20  
 ; PRIOR APPLICATION NUMBER: US/09/851,673  
 ; PRIOR FILING DATE: 2001-05-08  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 5371  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (392)..(3262)  
 ; US-10-760-678-3

## Alignment Scores:

Pred. No.:	0	Length:	5371
Score:	4971.50	Matches:	948
Percent Similarity:	99.16%	Conservative:	0
Best Local Similarity:	99.16%	Mismatches:	1
Query Match:	98.76%	Indels:	7
DB:	61	Gaps:	5

US-09-671-687a-3 (1-949) x US-10-760-678-3 (1-5371)

QY	1	MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgile	20
DB	392	ATGAGTTTCAGGCTTATGAGCCCAAGAAAAGTCATTCACCTACTGGGAAGCGGATT	451
QY	21	PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys	40
DB	452	TTTTTACTTGTCTTCAAGAAATGACAGCTTACAGACAAACAAACACAAAAGCTCTTAAA	511
QY	41	ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgile	60
DB	512	GTACCGAAGGGAAGATAGGACAGTATATTCAGATGCTTCTGTGGGCAATTCGAAGGATT	571
QY	61	ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla	80
DB	572	CTTCTCGAAAAGGCAAGAAAATCAGATTGGATTAAAAATTCAGACCACTCATGCA	631
QY	81	ValLeuPheValAspGlu---AspValValGluLeuAsnGluLysPheThrGluLeu	99
DB	632	GTTCTCTTTGTTGATGAAAAGGATGTTGTAGAGATAAATGAAAAGTTTCACAGAGTTACTT	691
QY	100	LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer	119
DB	692	TTGGCAATTAACCAATGTGAGGAGAGGTTTCAGCTGTTTAAAAACAGAAAACAGACTAAGT	751
QY	120	LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu	139
DB	752	AAAGCCCTCCAAATAGACGTGGGCTGTCCTGTGAAGTACAGCTGAGATCTGGGGAAGAA	811
QY	140	LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly	159
DB	812	AAATTTCTCGAGTTGTACGCTTCAGAGGACCCCTGTTAGCAGAGAGACAGTCTCCGGA	871
QY	160	IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal	179
DB	872	ATATTTCTTGGAGTTGAATTTCTCGAAGAAGGTCGTGCTCAAGGTTTTCACCTGACGGGGTG	931
QY	180	TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp	198
DB	932	TACCAGGGAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGGTGTTGTTCATTTGGAC	991
QY	199	LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly	218
DB	992	AAGCTAGAACTCATAGAAGATGATGACACTGCATTTGGAAAGTGATTACGACAGGTCCTGGG	1051

QY	219	AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly	238
DB	1052	GACACAATGCAGGTCGAACCTTCTCTTTGGAAATAACTCCAGAGTTCTTTGAAGTT	1111
QY	239	GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer	258
DB	1112	GGAGAAACAATAGAAATCTGGAACAGTTATTTCTGTGATGTTTTCGACGAAAAGAAC	1171
QY	259	LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe	278
DB	1172	TTAGGATATTTTGTGGTGTGACATGATACCCCTATTGGCAACTGGGATGGAAGATT	1231
QY	279	AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn	297
DB	1232	GATGGAGTGCAGCTTTGTAGTTTTCGGTGTGTTGAAAGTACAAATCTATTGCACATCAAT	1291
QY	298	AspIleIlePro-----GluSerValThrGlnGluArgArgProProLysLeuAla	314
DB	1292	GATATCATCCAGCTTTTATCAGAGAGTGTGACGCAAGAAAGGAGGCTCCCAAACTTGC	1351
QY	315	PheMetSerArgGlyValGlyAspLysGlySerSerSerHisAsnLysProLysAlaThr	334
DB	1352	TTTATGTCAGAGGTTTGGGACAAAGGTTTCATCCAGTCATAATAAAACCAAGGCTACA	1411
QY	335	GlySerThrSerAspProGlyAsnArg--ArgSerGluLeuPheTyrThrLeuAsnGly	353
DB	1412	GGATCTACTCAGACCTTGGAAANTAGAAACAGATCTGAATTTATTTATACCTTAAATGGG	1471
QY	354	SerSerValAspSerSerGlnSerLysSerLysAsnThrTrpTyrIleAspGluVal	373
DB	1472	TCTTCTGTTGACTCACACCAACCAATCCAAATCAAAATAATACATGTTGATGAAGTT	1531
QY	374	AlaGluAspProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerPro	393
DB	1532	GCAGAAGACCTTGCAAAATCTCTTACAGAGATATCTACAGACTTTTGACCGTTCTTCA	1591
QY	394	ProLeuGlnProProValAsnSerLeuThrGluAsnArgPheHisSerLeuPro	413
DB	1592	CCACTCCAGCTCTCTCTGTGAACCTCACTGACCAACGAGAAACAGATTCACCTCTTTACCA	1651
QY	414	PheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeu	433
DB	1652	TTGAGTCTCACCAAGATGCCCAATACCAATGGAAGTATTGGCCACAGTCCACTTCTCTG	1711
QY	434	SerAlaGlnSerValMetGluGluLeuAsnThrAlaProValGlnGluSerProLeu	453
DB	1712	TCAGCCAGTCTGTAATGGAAGAGCTAAACACTGACCCGCTCCAAAGAGAGTCCACCCCTG	1771
QY	454	AlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGlu	473
DB	1772	GCCATGCTCTCTGGGAACCTCACATGGTCTAGAAGTGGGCTCATTTGGCTGAAGTTAAGGAG	1831
QY	474	AsnProProPheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluVal	493
DB	1832	AAACCTCTCTTATGGGTAAATCGTTGGATCGTTCAGCCACAGGACTGAATGAAGTG	1891
QY	494	LeuAlaGlyLeuGluLeuAspGluCysAlaGlyCysThrAspGlyThrPheArgGly	513
DB	1892	CTCGCTGAGCTGGAACCTGGAAGATGAGTGTGAGGCTGTACGATGGAACCTTCAGAGGC	1951
QY	514	ThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArg	533
DB	1952	ACTCGGTATTTTACCTGTGCCCTGGAAGAGGCGCTGTTGTGTAACCTGAAGAGCTGCAGG	2011
QY	534	ProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSer	553
DB	2012	CCTGACTCTAGTTTGCATCATTTGCAGCCGCTTCCCAATCAGATTCAGGCGCTGTAACCT	2071
QY	554	LeuAlaPheGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGlu	573
DB	2072	TTAGCATTTGGAGGCTACTTAAAGTGAAGTAGTAGAAGAAAATACTCCACCAAAAATGGAA	2131
QY	574	LysGluGlyLeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSer	593



Db 2132 AAGAAGGCTTGGAGATAAATGATTGGGAAGAAAGGCATCCAGGGTCATTACAATTCT 2191  
QY CysTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrVal 613  
Db 2192 TGTACTTAGACTCAACCTTATCTGCTTATTTGCTTTAGTCTGTTCTGGACACTGTG 2251  
QY LeuLeuArgProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeu 633  
Db 2252 TTACTTAGACCCAAAGAAAGAACGATGTAGATATTATAGTGAACCCAGAGCTACTG 2311  
QY ArgThrGluLeuValAsnProLeuArgLleTyrGlyTyrValCysAlaThrLysIleMet 653  
Db 2312 AGACAGAAATGTTAATCTCTGAGAAATATGATATGATGTGTGTCACAAAATATG 2371  
QY LysLeuArgLysIleLeuGluLysValGluAlaAlaSerGlyPheThrSerGluGluLys 673  
Db 2372 AACTGAGGAATACTTGAAGGTGGAGCTGCATCAGGATTTACTCTGAAGAAAA 2431  
QY AspProGluLeuPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeu 693  
Db 2432 GATCCTGAGGAATCTTGAATATCTGTTTCATCATATTTAAGGGTAGAACCTTTGCTA 2491  
QY LysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGlu 713  
Db 2492 AAAATAAGATCAGCAGGTCAAAAGGTACAAGATTGTTACTCTATCAAAATTTTATGGAA 2551  
QY LysAsnGluLysValGlyValProThrIleGlnLeuLeuGluTyrSerPheIleAsn 733  
Db 2552 AAAAATGAGAAGTGGCGTTCCCAAAATTCAGCAGTTGTAGAAATGGTCTTTTATCAAC 2611  
QY SerAsnLeuLysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGly 753  
Db 2612 AGTAACCTGAAATTCGAGAGGCACCATCATGTCGATTATTCAGATGCTCGATTTGGA 2671  
QY LysAspPheLysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeu 773  
Db 2672 AAAGACTTTAAACTATTTAAAAAAATTTTCTCTCTCGAATTAATAACAGATTTA 2731  
QY LeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArg 793  
Db 2732 CTTGAAGACACTCCCAAGACTGCCGATATGTGGAGGGCTTGCATGTATGATGTGAGA 2791  
QY GluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCys 813  
Db 2792 GAATGCTACGACGATCCGGACATCTCAGCTGGAAAAATCAAGCAGTTTGTGTAACCTGC 2851  
QY AsnThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeu 833  
Db 2852 AACACTCAAGTCCACTTCATCCGAAGAGGCTGAATCATATAATATAACCCAGTGTCACTT 2911  
QY ProLysAspLeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGlu 853  
Db 2912 CCCAAAGACTTACCCGACTGGGACTGGAGACAGGCTGCATCCTCTGCCAGATATGGAG 2971  
QY LeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLys 873  
Db 2972 TTATTGCTGTTCTCTGCTAGAAAAACAAGCCATATGTTCTTTGTGAAGTAGTGGGAAG 3031  
QY AspAspSerAlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGly 893  
Db 3032 GACGATTCTGCTGGCTCTCTTTGTGACAGCATGGCCGATGGGTGATGATGGC 3091  
QY PheAsnIleProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeu 913  
Db 3092 TTCACATCTCTCAAGTCAACCCATGCCAAGAGTAGGAGACTTTGAAGATGTCTCTG 3151  
QY GluAspLeuHisSerLeuAspSerArgArgIleGlnGlyCysAlaArgLeuLeuCys 933  
Db 3152 GAAGACCTGCTATCTTGGACTCCAGAGAAATCCAAGGCTGTGCAAGACTGCTTTGT 3211  
QY AspAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949

Db 3212 GATGCATATATGTGCATGTACAGAGTCCAACAATGAGTTTGTACAAA 3259  
RESULT 21  
US-10-887-553A-199  
; Sequence 199 Application US/10887553A  
; GENERAL INFORMATION:  
; APPLICANT: Garza, Dan  
; APPLICANT: Li, Hao  
; TITLE OF INVENTION: Method to treat conditions associated  
; with insulin signalling dysregulation  
; FILE REFERENCE: 4-33262  
; CURRENT APPLICATION NUMBER: US/10/887,553A  
; CURRENT FILING DATE: 2004-07-08  
; PRIOR APPLICATION NUMBER: 60/485,883  
; PRIOR FILING DATE: 2003-08-07  
; NUMBER OF SEQ ID NOS: 1208  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 199  
; LENGTH: 5371  
; TYPE: DNA  
; ORGANISM: human  
US-10-887-553A-199  
Alignment Scores:  
Pred. No.: 0 Length: 5371  
Score: 4971.50 Matches: 948  
Percent Similarity: 99.16% Conservative: 0  
Best Local Similarity: 99.16% Mismatches: 1  
Query Match: 98.76% Indels: 7  
DB: Gaps: 5  
US-09-671-687A-3 (1-949) x US-10-887-553A-199 (1-5371)  
QY 1 MetSerSerGlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluLeuArgIle 20  
Db 392 ATGAGTTTCAGGCTTATGGAGCCAAAGAAAGTCACTTCACCTACTTGGAGAGCGGATT 451  
QY 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40  
Db 452 TTTTACTTGTCTTCTCAAGATGCGCTTACAGCAAAACAAACAAAGTCTCTTAAA 511  
QY 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60  
Db 512 GTACCGAAGGGAAGTATAGGACAGATATATTCAAGATCGTCTCTGTGGGCATTTCAAGATT 571  
QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80  
Db 572 CCTTCTCAAAAGCAAGAAAAATCAGATTGGATTAAAAATTTAGAGCAACCTCATGCA 631  
QY 81 ValLeuPheValAspGlu---AspValValGluLeuAsnGluLysPheThrGluLeuLeu 99  
Db 632 GTTCTCTTGTGTGATGAAAAGGATGTTGTAGAGATAAATGAAAAGTTTCAAGAGTTACTTT 691  
QY 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119  
Db 692 TTGGCAATTACCAATTGTGAGAGAGGTTGAGCCTGTTTAAAAACAGAAACAGACTAAGT 751  
QY 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139  
Db 752 AAAGGCTCCAAATAGACGTGGGTGCTCTGTGAAAAGTACAGCTGAGATCTGGGGAAGAA 811  
QY 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159  
Db 812 AAATTTCTCTGGAGTTGATCGCTTCAGAGGACCCCTGTTAGCAGAGAGACAGTCTCCGGA 871  
QY 160 IlePhePheGlyValGluLeuLeuGluGluGlyGlnGlyPheThrAspGlyVal 179  
Db 872 ATATTCTTGGAGTTGAATTTGCTGGAAGAGGTCGTGGTCAAGGTTTCACTGACCGGGTG 931  
QY 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198  
Db 932 TACCAGGGAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTCTTTGTTCATTTGGAC 991

QY	199	LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly	218		Db	2072	TTAGCATTTGGAGGCTACTTAAGTGAAGTGAAGAAATACTCCACCAAAATGGAA	2131	
Db	992	AAGCTAGAACTCATAGAAGATGATGACATGCAATTGGAAAAGTATTACGCAGGTCCTGGG	1051		QY	574	LysGluGlyLeuGluIleMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSer	593	
QY	219	AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly	238		Db	2132	AAAGAAGGCTTGGAGATTAATGATGGGAAGAAGAACGATCCAGGGTCATTACAAATCT	2191	
Db	1052	GACAAATGAGGTCGAACCTTCCTCTTGGAAATAAATCCAGAGTTCTTTGAAGGTT	1111		QY	594	CysTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrVal	613	
QY	239	GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer	258		Db	2192	TGTTACTTAGACTCAACCTTATCTGCTTATTTGCTTTTAGTTCTGTTCTGGACACTGTG	2251	
Db	1112	GGAAACAATAGNAATCTGGACAGTTATATCTGTGATGTTTGGCCAGGAAGAAGC	1171		QY	614	LeuLeuArgProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeu	633	
QY	259	LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe	278		Db	2252	TTACTTAGACCCCAAGAAAGAACGATGTAGAAATATTATAGTGAACCAACGAGCTACTG	2311	
Db	1172	TTAGGATATTTTGTGTGTGGACATGGATAACCTATTGGCAACTGGGATGGAGATTT	1231		QY	634	ArgThrGluIleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMet	653	
QY	279	AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn	297		Db	2312	AGGACAGAAATTTGTAATCTCTGAGAAATATATGGATATGTGTGCCACAAAAATTATG	2371	
Db	1232	GATGGAGTGCAGCTTGTAGTTTTTGCCTGTGTGAAAGTACAAATCTATTTCACATCAAT	1291		QY	654	LysLeuArgLysIleLeuGluLysValGluAlaAspSerGlyPheThrSerGluGluLys	673	
QY	298	AspIleIlePro-----GluSerValThrGlnGluArgArgProProLysLeuAla	314		Db	2372	AAACTGAGAAAATACTTTGAAAAGGTGGAGGCTGCATCAGGATTTTACCTCTGAAGAAAA	2431	
Db	1292	GATATCATCCAGCTTATCATGAGAGTGTGACGAGGAAGAGGCGCTCCCAAACTTGCC	1351		QY	674	AspProGluGluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeu	693	
QY	315	PheMetSerArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThr	334		Db	2432	GATCCTGAGGAATTTCTTGAATATTCTGTTTCATCATATTTTAAGGGTAGAACCTTTGCTA	2491	
Db	1352	TTTATGTCAAGAGTGTGGGACAAAGTTTCATCCAGTCAATAATAACCAAGGCTACA	1411		QY	694	LysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGlu	713	
QY	335	GlySerThrSerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGly	353		Db	2492	AAAAATAAGATCAGCAGGTCAAAAGGTACAAGATTGTACTTCTATCAAAATTTTATGGAA	2551	
Db	1412	GGATCTACCTCAGACCCCTGGAAATAGAAAACAGATCTGAATTTATTTTATACCTTAATGGG	1471		QY	714	LysAsnGluLysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsn	733	
QY	354	SerSerValAspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluVal	373		Db	2552	AAAAATGAGAAAGTTGGCGTTCCCAAAATCAGCAGTTGTAGAAATGGTCTTTTATCAAC	2611	
Db	1472	TCCTCTGTGACTCACAAACCAATCAAAATCAAAATAATCATGGTACATTTGATGAAGTT	1531		QY	734	SerAsnLeuLysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGly	753	
QY	374	AlaGluAspProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerPro	393		Db	2612	AGTAACCTGAAATTTGCAGAGGCACCATCATGTCGTATTTTTCAGATGCTCGATTTGGA	2671	
Db	1532	GCAGAAACCTCGAAAATCTCTTACAGAGATATCTACAGACTTTGACCGTTCTTCACCA	1591		QY	754	LysAspPheLysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeu	773	
QY	394	ProLeuGlnProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuPro	413		Db	2672	AAAGACTTTAAACTATTATAAAAAATTTTCTCTCTGGAATTTAAATATAACAGATTTA	2731	
Db	1592	CCATCTCAGCCTCTCTCTGTAACCTCACTGACCCAGGAGACAGATCCCACTCTTTACCA	1651		QY	774	LeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArg	793	
QY	414	PheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeu	433		Db	2732	CTTGAAGACACTCCACAGACAGTCCGGATATGTGGAGGCTTGCATATGTATCAGTGTAGA	2791	
Db	1652	TTCACTCTCAACAGATGCCAATACCAATGGAAGTATTGGCCACAGTCCCACTTTCTCTG	1711		QY	794	GluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCys	813	
QY	434	SerAlaGlnSerValMetGluLeuLeuAsnThrAlaProValGlnGluSerProProLeu	453		Db	2792	GAATGTCTACGACGATCCGGACATCTCAGCTGGAAAAAATCAACGAGTTTTTGTAAAACCTGC	2851	
Db	1712	TCAGCCCACTCTGTAATGGAAAGACTAAACACTGCACCCGTCGAAGAGAGTCCACCCCTTG	1771		QY	814	AsnThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeu	833	
QY	454	AlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGlu	473		Db	2852	AAACTCAAGTCCACCTTTCATCCGAAGAGGCTGAATCATATAATAACCCAGTGCACCT	2911	
Db	1772	GCCATGCTCTCTGGAACTCATAGTGTCTAGAAAGTGGGCTCATTTGGCTGAAGTTAAGAG	1831		QY	834	ProLysAspLeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGlu	853	
QY	474	AsnProProPheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluVal	493		Db	2912	CCCAAGACTTACCCGACTGGGACTGGAGACACGCTGCATCCCTTGCAGAAATATGGAG	2971	
Db	1832	AAACCTCTTCTATGGGGTAATCCGTTGGATCGGTCAAGCCAGCCAGGACTGAATGAAGTG	1891		QY	854	LeuPheAlaValLeuLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLys	873	
QY	494	LeuAlaGlyLeuLeuLeuAspGluCysAlaGlyCysThrAspGlyThrPheArgGly	513		Db	2972	TTATTTGCTGTCTCTGCTAGAAAACCAAGCCACTATGTTGCTTTTGTGAAGTATGGGAAG	3031	
Db	1892	CTCGCTGGACTGGAACTGGGAAGATGAGTGTGCAGGCTGTACGGATGGAACTTCAGAGGC	1951		QY	874	AspAspSerAlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGly	893	
QY	514	ThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArg	533		Db	3032	GACGATTTCTGCTGCTCTTCTTTGACAGCATGGCCGATCGGATGGTGGTTCAGAAATGCG	3091	
Db	1952	ACTCGGTATTTCACTGTGCTCTGAGAGAGCGCTGTTTGTGAACCTGAAGAGCTGCAGG	2011		QY	894	PheAsnIleProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeu	913	
QY	534	ProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSer	553		Db	3092	TTCAACATTTCTCAAGTCAACCCATGCCAGAGTAGGAGAGTACTTGAAGATGTCTCTG	3151	
Db	2012	CCTGACTCTAGTTTGCATCATTTGCAGCGGTTTCCAATCAGATTGAGCGCTGTAACCTCT	2071		QY	914	GluAspLeuHisSerLeuAspSerArgIleGlnGlyCysAlaArgLeuLeuCys	933	
QY	554	LeuAlaPheGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGlu	573						

Db 3152 GAAGACCTGCATTCCTTGGACTCCAGAGAAATCAAGGCTGTGCACGAAGACTCCTTTGT 3211  
 QY 934 AspAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949  
 Db 3212 GATGCATATATGTGATGTACCGAGAGTCCAACAATGAGTTGTACAAA 3259

## RESULT 22

US-60-440-068-489  
 ; Sequence 489, Application US/60440068  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NADLER, STEVEN G.  
 ; APPLICANT: CARMAN, JULIE  
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE  
 ; FILE OF INVENTION: NF-KB PATHWAY  
 ; FILE REFERENCE: 3053-4191  
 ; CURRENT APPLICATION NUMBER: US/60/440,068  
 ; CURRENT FILING DATE: 2003-01-14  
 ; NUMBER OF SEQ ID NOS: 746  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 489  
 ; LENGTH: 5371  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-60-440-068-489

Alignment Scores:  
 Pred. No.: 0 Length: 5371  
 Score: 4971.50 Matches: 948  
 Percent Similarity: 99.16% Conservative: 0  
 Best Local Similarity: 99.16% Mismatches: 1  
 Query Match: 98.76% Indels: 7  
 DB: 79 Gaps: 5

US-09-671-687A-3 (1-949) x US-60-440-068-489 (1-5371)

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 Db 392 ATGAGTTTCAGGCTTATGGAGCCCAAGAAAAGTCACTTCCCTACTTGGGAAGCGGATT 451  
 QY 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40  
 Db 452 TTTTACTTCTCTTCAAGAATGCAGCTTACAGACAAAACAAAACACAAAAGCTCTTAAA 511  
 QY 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60  
 Db 512 GTACCGAAGGGAAGTATAGACAGTATATTCAGATCGTTCTGTGGGCAATTCAGGATT 571  
 QY 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnProHisAla 80  
 Db 572 CCTTCTGCAAAAGGCAAGAAAATCAGATTGGATTAAATAATTCAGAGCAACCTCATGCA 631  
 QY 81 ValLeuPheValAspGlu---AspValValGluLeuAsnGlnLysPheThrGluLeuLeu 99  
 Db 632 GTTCTCTTTTGTGATGAAAGGATGTTAGAGATAAATGAAAGTTTACAGAGTTACTT 691  
 QY 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119  
 Db 692 TTGGCAATTACCATTGTGAGGAGAGGTTGAGGCTGTTTAAATAACAGAAACAGACTAAGT 751  
 QY 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139  
 Db 752 AAAGGCTCCAAATAGACGCTGGGCTGCTGTGAAAGTACAGCTGAGATCTGGGGAGAA 811  
 QY 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159  
 Db 812 AAATTTCTCTGGAGTTGATCGCTTCAGAGACCCCTGTAGCAGAGGACAGTCTCCGGA 871  
 QY 160 IlePhePheGlyValGlnLeuLeuGluGluArgGlyGlnGlyPheThrAspGlyVal 179  
 Db 872 ATATTCTTTGGAGTTGAATGTCTGGGAAGAGGTCGTGGTCAAGGTTTCTACTGACGGGGT 931  
 QY 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198  
 Db 932 TACCAAGGGAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTTCCTTCATTTGGAC 991  
 QY 199 LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218  
 Db 992 AAGCTAGAACTCATAGAAGATGATGACACTGCATTTGGAAGTGATTACGACGGTCTCTGG 1051  
 QY 219 AspThrMetGlnValGluLeuProLeuGluIleAsnSerArgValSerLeuLysGly 238  
 Db 1052 GACACAATGCAGGTCGAACCTTCTCTTGTGAAATAAACTCCAGAGTTTCTTTGAAGGTT 1111  
 QY 239 GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258  
 Db 1112 GGAGAAACAATAGAAATCTGSAACAGTTATATTCGTGTGATGTTCAGCAAGAAAGAAC 1171  
 QY 259 LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTyrAspGlyArgPhe 278  
 Db 1172 TTAGGATATTTTGTGTGTGGACATGATTAACCTATTTGGCACTGGGATGGAGATT 1231  
 QY 279 AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297  
 Db 1232 GATGAGTGCAGCTTTGTAGTTTTCGTGTGTTGAAAGTACAAATCTATTGCACATCAAT 1291  
 QY 298 AspilelePro-----GluSerValThrGlnGluArgArgProProLysLeuAla 314  
 Db 1292 GATATCATCCAGCTTTATACAGAGAGTGTGACGAGAAAGAGGCGCTCCCAAACTGCC 1351  
 QY 315 PheMetSerArgGlyValGlyAspLysGlySerSerSerHisAsnLysProLysAlaThr 334  
 Db 1352 TTTATGTCAGAGGTTTGGGACAAGGTTTCATCCAGTCATAATAAACCAAGGCTACA 1411  
 QY 335 GlySerThrSerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGly 353  
 Db 1412 GGATCTACCTCAGACCCCTGGAAATAGAAACAGATCTGAATTTATTTATACCTTAATGG 1471  
 QY 354 SerSerValAspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluVal 373  
 Db 1472 TCTTCTGTGACTCACAACCAATCCAAATCAAAATACATAATGATGATGATGATGATGAT 1531  
 QY 374 AlaGluAspProAlaLysSerLeuThrGluLeuSerThrAspPheAspArgSerPro 393  
 Db 1532 GCAGAAACCCCTGCATAATCTCTTACAGAGATATCTACAGACTTTTGACCGTTCCTCACA 1591  
 QY 394 ProLeuGlnProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuPro 413  
 Db 1592 CCATCCAGGCTCTCTCTGTGAATCTACTGACCCAGGAGACAGATTCCACTCTTTTACCA 1651  
 QY 414 PheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeu 433  
 Db 1652 TTCAGTCTCACCAGATGCCCAATACCAATGGAAGTATTGGCCACAGTCCACTTTCTCTG 1711  
 QY 434 SerAlaGlnSerValMetGluLeuLeuAsnThrAlaProValGlnGluSerProLeu 453  
 Db 1712 TCAGCCAGCTGTGTAATGGAAGAGCTAAACACTGCACCCGTCGAAGAGATCCACCTTG 1771  
 QY 454 AlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGlu 473  
 Db 1772 GCCATGCTCTGGAACTCACATGGTCTAGAGTGGGCTCATTTGGCTGAAGTTAAGAG 1831  
 QY 474 AsnProProPheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluVal 493  
 Db 1832 AACCTCTCTTCTATGGGTAATCCGTTGGATCGTCAGCCACCAGGACTGAATGAAGTG 1891  
 QY 494 LeuAlaGlyLeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGly 513  
 Db 1892 CTCGCTGCAGTGGAACTGGAAGATGAGTGTGCGAGCTGTACGGATGGAACCTTCAGAGGC 1951  
 QY 514 ThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArg 533  
 Db 1952 ACTCGGTATTTTCACTGTGCCCTGGAAGAGCGCTGTTTGTGAAACTGAAGAGCTGCGAG 2011  
 QY 534 ProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSer 553  
 Db 2012 CCTGACTCTAGTTTGCATCATTCAGCCCGGTTTCCAAATCAGATTGAGCGCTGTAACTCT 2071

Qy 554 LeuAlaPheGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGlu 573  
Db 2072 TTAGCATTTTGGAGCTACTTAAAGTAGAAGAGAAATACTCCACCAAAATGGAA 2131  
Qy 574 LysGluGlyLeuGluIleMetIleGlyLysLysGlyGlyLeuGlnGlyHisTyrAsnSer 593  
Db 2132 AAAGAAGGCTTGGAGATAATGATTTGGGAAGAAAGGCATCCAGGCTCATTAATTTCT 2191  
Qy 594 CysTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerValLeuAspThrVal 613  
Db 2192 TGTACTTAGACTCAACCTTATTTCTGTTATTTGCTTTTAGTTCTGTTCTGGACACGTG 2251  
Qy 614 LeuLeuArgProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeu 633  
Db 2252 TTACTTAGACCCAAAGAAAGACGATGATAGATATTTATAGTGAACCCCAAGAGCTACTG 2311  
Qy 634 ArgThrGluIleValLeuProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMet 653  
Db 2312 AGACAGAAATTTGTAATCTCTGAGAAATATATGATATGTTGTGTGCCACAAATTTATG 2371  
Qy 654 LysLeuArgLysIleLeuGluLysValGluAlaSerGlyPheThrSerGluGluLys 673  
Db 2372 AAATGAGGAAATACTTTGAAAGGTGGAGCTGCATCAGATTTACTCTGAGAAATAA 2431  
Qy 674 AspProGluGluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeu 693  
Db 2432 GATCCTGAGGAATCTTGAATATTTCTGTTTCATCATATTTTAAAGGTAGAACCTTCTG 2491  
Qy 694 LysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGlu 713  
Db 2492 AAAATAAGATCAGCAGGTCAAAAGGTCAAGATTTGTTACTTCTATCAAAATTTTATGAA 2551  
Qy 714 LysAsnGluLysValGlyValProThrIleGlnLeuLeuGluTyrSerPheIleAsn 733  
Db 2552 AAAAATGAGAAAGTTGGCGTTCCACAAATTCAGCAGTTGTTAGAAATGCTCTTTATCAAC 2611  
Qy 734 SerAsnLeuLysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGly 753  
Db 2612 AGTAACCTGAAATTTGCAGAGGACCATCATCTGATTAATTCAGATGCCTCGATTTGGA 2671  
Qy 754 LysAspPheLysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeu 773  
Db 2672 AAAGACTTTAAACTATTTAAATAAAATTTTCTCTCGAAATTAATAATAACAGATTTA 2731  
Qy 774 LeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArg 793  
Db 2732 CTTGAAGACACTCCACACAGTCCGGATATGTGGAGGCTTGCATATGATGATGTAGA 2791  
Qy 794 GluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCys 813  
Db 2792 GAATGCTACGACGATCCGGACATCTCAGCTGGAAATAACAAGCAGTTTGTAAACCTCGC 2851  
Qy 814 AsnThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeu 833  
Db 2852 AACACTCAAGTCCACCTTTCATCCGAAGAGCTGATCATATAATAACCCAGTGTCACTT 2911  
Qy 834 ProLysAspLeuProAspThrAspThrArgHisGlyCysIleProCysGlnAsnMetGlu 853  
Db 2912 CCCAAAGACTTACCCGACTGGAGACACGGCTGCATCCCTTCCAGAAATATGGAG 2971  
Qy 854 LeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLys 873  
Db 2972 TTAATTTGCTCTCTCTGCAATAGAAACAAAGCCACTATGTTGTTGAAAGATATGGGAG 3031  
Qy 874 AspAspSerAlaThrLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGly 893  
Db 3032 GACGATTCGCTGGCTCTCTTTTGACAGCATATGGCCGATCGGATGTTGTCAGAAATGGC 3091  
Qy 894 PheAsnIleProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeu 913  
Db 3092 TTCAACATCTCTCAAGTCACCCCATGCCAGAGTAGGAGAGTACTTGAAGATGCTCTG 3151

Qy 914 GluAspLeuHisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCys 933  
Db 3152 GAAGACCTGCATCTCTTGGACTCCAGGAGATCCAAAGCTGTGCAGAGACTGCTTTGT 3211  
Qy 934 AspAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949  
Db 3212 GATGCATATATGTCATGTACCGAGTCCAAACATAGTTTGTATCAAA 3259  
RESULT 23  
US-60-469-757-489  
; Sequence 489, Application US/60469757  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB  
; FILE REFERENCE: D0284 PSp1  
; CURRENT APPLICATION NUMBER: US/60/469,757  
; CURRENT FILING DATE: 2003-05-12  
; NUMBER OF SEQ ID NOS: 823  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 489  
; LENGTH: 5371  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-469-757-489  
Alignment Scores:  
Pred. No.: 0 Length: 5371  
Score: 4971.50 Matches: 948  
Percent Similarity: 99.16% Conservative: 0  
Best Local Similarity: 99.16% Mismatches: 1  
Query Match: 98.76% Indels: 7  
DB: 80 Gaps: 5  
US-09-671-687A-3 (1-949) x US-60-469-757-489 (1-5371)  
Qy 1 MetSerSerGlyLeuTyrSerGlnGluLysValThrSerProTyrTrpGluGluArgile 20  
Db 392 ATGAGTTTCAGGCTTATGGAGCCAAAGAAAGTCACTTCCCTACTTGGGAAGCGGATT 451  
Qy 21 PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLys 40  
Db 452 TTTTACTTGTCTTCTCAAGATGCGGCTTACAGACAAACAAACACAAAGCTCCTTAA 511  
Qy 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgile 60  
Db 512 GTACCGAAGGGAAGTATAGGACAGTATATCAAGATCTTCTGTGGGCAATTCAGAGATT 571  
Qy 61 ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla 80  
Db 572 CCTTCTGCNAAGGCAAGAAATTCAGATTGGATTAATAATCTAGAGCACTCATGCA 631  
Qy 81 ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99  
Db 632 GTTCTCTTTGTTGATGAAAGGATGTTGTAGAGATAAATGAAAGTTTCAAGAGTTACTT 691  
Qy 100 LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119  
Db 692 TTGCAATTAACCAATTTGTAGAGAGGTTTCAGCTGTTTAAATAACAGAAACAGACTAAGT 751  
Qy 120 LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139  
Db 752 AAAGCCTCCAAATAGACGTGGGCTGCTCTGTGAAGTACAGTCAGATCTGGGGAAGAA 811  
Qy 140 LysPheProGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGly 159  
Db 812 AAATTTCTCGAGTTGTACGCTTCAGAGGACCCCTGTTTAGCAGAGAGGACACTCCGGA 871  
Qy 160 IlePhePheGlyValGluLeuLeuGluGlnGlyArgGlyGlnGlyPheThrAspGlyVal 179  
Db 872 ATATCTTTTGGAGTTGAATTTCTCGAAGAGGTCGTGTCTCAAGGTTTCACTACGCGGTTG 931  
Qy 180 TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198

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932  TACCAAGGGAACACGCTTTTTCAGTGTGATGAAGATTGTGGCGGTGTTGTGCAATTGGAC 991
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Db  GACACAATGCGAGTGCAGACTTCTCTCTTGGAAATAAACTCCAGAGTTCTCTTGAAGGTT 1111
QY  GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
Db  GGAAGAACATAGAACTGGAACAGTTATATCTGTGATGTTTGGCAGGAAAGAAAGC 1171
QY  LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
Db  TTAGGATATTTGTTGGTGTGACATGATTAACCTTATTTGGCACTGGATGGAGATTT 1231
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Db  GATGGAGTGCAGCTTTGTAGTTTGGCTGTGTTGAAAGTACAATTCTTATTGCATCAAT 1291
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Db  TTTATGTCAAGAGGTGTTGGGCAAGAGTTTCATCCAGTCAATAAACCAGGCTGACA 1411
QY  GlySerThrSerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGly 353
Db  GGATCTACCTCAGACCCCTGGAATAGAAACAGATCTGAATTATTTATATCTTAAATGGG 1471
QY  SerSerValAspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluVal 373
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QY  AlaGluAspProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerPro 393
Db  GCAGAAGACCCCTGCAAAATCTCTTACAGAGATATCTACAGACTTTGACCGTCTTCCACA 1591
QY  ProLeuGlnProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuPro 413
Db  CCACCTCCAGCTCTCTCTGTGAATCTACTGACCAACCGAGAACAGATTCCACTCTTTACCA 1651
QY  PheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeu 433
Db  TTCAGTCTCACCAAGATGCCAATACCAATGGAAGTATTGGCCACAGTCCACTTTCTCTG 1711
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QY  AlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGlu 473
Db  GCCATGCCCTCTGGGAACCTCACATGGTCTAGAAGTGGGCTCATTTGGCTGAAGTAAAGAG 1831
QY  AsnProProPheTyrGlyValIleArgTyrIleGlyGlnProProGlyLeuAsnGluVal 493
Db  AACCTCTCTTCTATGGGTAAATCCGTTGGATCGGTGAGCCACGAGGACTGAATGAAGTG 1891
QY  LeuAlaGlyLeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGly 513
Db  CTCGCTGGACTGGAACCTGGAAGATGAGTGTGCGAGGCTGTACGGATGGAACCTTCAGAGGC 1951
QY  ThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArg 533
Db  ACTCGGTATTTACCTGTGCGCTTGAAGAGGCGCTGTTGTGAAACTGAAGAGCTGCAGG 2011
QY  ProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSer 553
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2012  CCTGACTCTAGGTTTGCATCATTTGCGAGCGCGTTTCCAAATCAGATTGAGCGCTGTAACCTCT 2071
QY  LeuAlaPheGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGlu 573
Db  TTAGCATTTGGAGGCTACTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAAATGGAA 2131
QY  LysGluGlyLeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSer 593
Db  AAAGAAGGCTTTGGAGATAATGATTGGGAAGAAAGGATCCAGGGTCAITTACAATTCT 2191
QY  CystTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrVal 613
Db  TGTACTTACCTCAACCTTATCTGCTTATTTGCTTTTAGTTCCTGTCGACACTGTG 2251
QY  LeuLeuArgProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeu 633
Db  TTACTTAGACCCAAAGAAAGAACGATGATAGATATATATAGTGAACCCAGAGCTACTG 2311
QY  ArgThrGluIleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMet 653
Db  AGGACAGAAATTTTAATCTCTGAGAATAATGATATGATGATGTTGTGTCACAAAATATG 2371
QY  LysLeuArgLysIleLeuGluLysValGluAlaIleAsnSerGlyPheThrSerGluLys 673
Db  AAACCTGAGGAAATACTTGAAGGTGGAGCTGCATCAGGATTTTACCTCTGAAGAAAA 2431
QY  AspProGluGluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeu 693
Db  GATCTCAGGAATTTCTTGAATATTTCTGTTTCATCATATTTTAAGGTTAGAACCTTTGCTA 2491
QY  LysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGlu 713
Db  AAAATAAGATCAGCAGGTCAAAAGGTCAAGATGTTTACTTCTATCAATTTTATGGAA 2551
QY  LysAsnGluLysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsn 733
Db  AAAAATGAGAAGTTGGCGTTCCACAAATTCAGCAGTTGTTAGAAATGCTTTTATCAAC 2611
QY  SerAsnLeuLysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGly 753
Db  AGTAACCTGAAATTTGAGAGGCCACCATCATGTCTGATTATTCAGATGCCCTCGATTGGA 2671
QY  LysAspPheLysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeu 773
Db  AAAGACTTTAAACTATTTTAAAAAATTTTCTCTCTGGAAATTAATAATATACAGATTGA 2731
QY  LeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArg 793
Db  CTTGAAGACACTCCACAGACAGTCCGGATATGTGGAGGCTTGGCAATGATGAGTGTAGA 2791
QY  GluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCys 813
Db  GAATGCTTACGACGATCCGACATCTCAGCTGGAAAAATCAAGCAGTCTTTTGTAAAAACCTGC 2851
QY  AsnThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeu 833
Db  AACACTCAAGTCCACCTTCATCCGAAGAGGCTGAATATAAATAATATAAACCCAGTGCATT 2911
QY  ProLysAspLeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGlu 853
Db  CCCAAAGACTTACCCGACTGGGACTGGAGACACCGCTGCATCCCTTGGCAGAAATATGAG 2971
QY  LeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLys 873
Db  TTATTTGCTGTTCTCTGCATAGAAACAAAGCAGCTATGTTGCTTTTGTGAAGTATGGGAAG 3031
QY  AspAspSerAlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGly 893
Db  GACGATTTCTCCCTGGCTCTTCTTTGACAGCATGCCCATCGGATGGGATGGGTGAGAAATGGC 3091
QY  PheAsnIleProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeu 913
Db  TTCAACATTCTCNAAGTCAACCCCATGCCAGAGTAGGAGAGTACTTGAAGATGTTCTCTG 3151
```

Qy	914	GlutAspLeuHisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCys	933
Db	3152	GAAGACCTGCAATTCCTTGGACTCCAGGAGATCCAAAGCTGTGCACGAAGACTGCTTTGT	3211
Qy	934	AspAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyrLys	949
Db	3212	GATGCATATATGTGCATGTACCAAGAGTCCAAACATGAGTTGTACAAA	3259

Db 1832 AACCTCCTTTCTATGGGGTAATCCGTTGGATCGGTGAGCCACCAGGACTGAATGAAGTG 1891  
QY 494 LeuAlaGlyLeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGly 513  
Db 1892 CTCGCTGGACTGGAACTGGGAAGATGAGTGTGACGGCTGTACGGATGGAACCTTCAGAGGC 1951  
QY 514 ThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArg 533  
Db 1952 ACTCGGTATTTCACCTGTGCCCTGAAGAAGCGCTGTTTGAACACTGAAGAGCTGCAGG 2011  
QY 534 ProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSer 553  
Db 2012 CCTGACTCTAGGTTTGCATTCATTCAGCGGTTTCCATCAGATTGAGCGCTGAACCTC 2071  
QY 554 LeuAlaPheGlyGlyTyrLeuSerGluValGluGluAsnThrProProLysMetGlu 573  
Db 2072 TTAGCAATTTGAGGCTACTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAA 2131  
QY 574 LysGluGluLeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSer 593  
Db 2132 AAAGAAGGCTTGGAGATAATGATTGGGAAGAAGAAAGGCATCCAGGGTCAATTACAATTCT 2191  
QY 594 CysTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrVal 613  
Db 2192 TGTACTTAGACTCAACCTTATTCTGCTTATTCTGTTTTAGTCTGTCTGGACACTGTG 2251  
QY 614 LeuLeuArgProLysGluLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeu 633  
Db 2252 TTACTTAGACCCAAAGAAAGACGATGTAGATATTATATAGTGAACCCAGAGCTACTG 2311  
QY 634 ArgThrGluIleValLeuProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMet 653  
Db 2312 AGCAGCAAAATGTTAATCTCTGAGAAATATATGATATGTTGTGTCACAAAAATATG 2371  
QY 654 LysLeuArgLysIleLeuGluLysValGluAlaSerGlyPheThrSerGluGluLys 673  
Db 2372 AAATCAGGAAATACTTGAAGAGGTGGAGCTGCATCAGGATTTACCTCTGAAGAAAA 2431  
QY 674 AspProGluGluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeu 693  
Db 2432 GATCCTGAGGAATCTTGAATATCTGTTTCATCATATTTTAAGGTAGAACCTTTGCTA 2491  
QY 694 LysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGlu 713  
Db 2492 AAAATAAGATCAGCAGTCAAAAGGTACAAGATTGTTACTTCTATCAAAATTTTATGGAA 2551  
QY 714 LysAsnGluLysValGlyValProThrIleGlnLeuLeuGluTrpSerPheIleAsn 733  
Db 2552 AAAAATGGAAAGTTGGCGTTCCCAAAATTCAGCAGTTGTAGAATGGTCTTTTATCAAC 2611  
QY 734 SerAsnLeuLysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGly 753  
Db 2612 AGTAACCTGAAATTCAGAGGCACCATCATGTCTGATTAATCAGATGCTCCGATTGGA 2671  
QY 754 LysAspPheLysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeu 773  
Db 2672 AAAGACTTTAAACTATTAAAAAAATTTTCTTCTGGAATTAATAACAGATTGA 2731  
QY 774 LeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArg 793  
Db 2732 CTTGAAGACACTCCACAGACGTCCGCGATATGTGGAGGGCTTGCATGTATGAGTGTGA 2791  
QY 794 GluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCys 813  
Db 2792 GAATGCTACGACATCCGACATCTCAGCTGGAAAAATCAAGCAGTTTTTGTAAAAACCTGC 2851  
QY 814 AsnThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeu 833  
Db 2852 AACACTCAAGTCCACCTTCATCCGAAGAGGCTGAATCATATAATTAACCCAGTGTCACT 2911  
QY 834 ProLysAspLeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGlu 853  
Db 2912 CCCAAAGACTTACCCGACTGGGACTGGAGACACGGCTGCATCCCTTGGCCAGATATGGAG 2971

QY 854 LeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLys 873  
Db 2972 TTAATTTGCTGTCTCTGCATAGAAACAAGCCACTATGTGTCTTTTGTGAAGTATGGAAG 3031  
QY 874 AspAspSerAlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGly 893  
Db 3032 GACGATTTCTGCTGGCTCTTCTTTGACAGCATGGCCGATCGCGATGGTGTGAGATGGC 3091  
QY 894 PheAsnIleProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeu 913  
Db 3092 TTCAACATTTCTCAAGTCACCCATGCCCAGAGATGAGAGAGTACTTGAAGATGTCCTCG 3151  
QY 914 GluAspLeuHisSerLeuAspSerArgIleGlnGlyCysAlaArgArgLeuLeuCys 933  
Db 3152 GAAGACCTGCATTCCTTGGACTCCAGGAGAAATCCAAGCTGTGCACGAAGACTGCTTTGT 3211  
QY 934 AspAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949  
Db 3212 GATCATATATGTGCATGTACCAGAGTCCAACAATGAGTTTTGTACAAA 3259

## RESULT 25

US-60-324-185-23812  
; Sequence 23812, Application US/60324185  
; GENERAL INFORMATION:  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Lal, Preeti  
; APPLICANT: Diep, Dinh  
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING  
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE  
; FILE REFERENCE: GX-0019-1 P  
; CURRENT APPLICATION NUMBER: US/60/324,185  
; CURRENT FILING DATE: 2001-09-21  
; NUMBER OF SEQ ID NOS: 35862  
; SOFTWARE: PERL Program  
; SEQ ID NO 23812  
; LENGTH: 6314  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No: 338326.5  
; NAME/KEY: unsure  
; LOCATION: 5941  
; OTHER INFORMATION: a, t, c, g, or other  
US-60-324-185-23812

Alignment Scores:  
Pred. No.: 0 Length: 6314  
Score: 4970.00 Matches: 945  
Percent Similarity: 99.47% Conservative: 0  
Best Local Similarity: 99.47% Mismatches: 1  
Query Match: 98.73% Indels: 4  
DB: 78 Gaps: 4

US-09-671-687A-3 (1-949) x US-60-324-185-23812 (1-6314)

QY 4 GlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIlePheTyrLeu 23  
Db 270 GGCTTATGGAGCCCAAGAAAAAGTCACTTCACTTCTGGAAGAGCGGATTTTCTTAC 329  
QY 24 LeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuValProLys 43  
Db 330 CTTCTTCAAGATGTCAGCGTTACAGACAAACAAACAAAGCTCTTAAAGTACCGAAG 389  
QY 44 GlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIleProSerAla 63  
Db 390 GGAAGTATAGGACAGATATATTCAAGATCGTGTCTGTGGGGCAATCAAGGATTCCTTCTGCA 449  
QY 64 LysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAlaValLeuPhe 83  
Db 450 AAAGGCAAGAAAAATCAGATTGGATTAAAAATCTAGGCAACCTCATGCACTTCTCTTT 509





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Db      2670 GACATCTCAGCTGGAAATAATCAAGCAGTTTTTTGTAATAACCTTGCACACTCAAGTCCACCTT 2729
QY      820 HisProLysArgLeuAenHisLysTyrAsnProValSerLeuProLysAspLeuProAsp 839
Db      2730 CATCCGAAGAGGCTGAATCATAATAATAACCCAGTGTCACTTCCCAAGACTTACCCTGAC 2789
QY      840 TrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAlaValLeuLysCys 859
Db      2790 TGGGACTGGAGACACCGCTGCATCCCTTGCAGAAATATGGAGTTATTGTGCTGTCTCTGC 2849
QY      860 IleGluThrSerHisTyrValAlaPheValLysTyrGlyGlnAsnGlyPheAsnIleProGlnVal 879
Db      2850 ATAGAAACCAAGCCACTATGTCTTTGTGAAGTATGGGAAGACGATCTCGCTCGCTC 2909
QY      880 PhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIleProGlnVal 899
Db      2910 TTCTTTGACAGCATGCGCATGGGATGGTGTGAGATGGCTTCAACATTTCTCAAGTC 2969
QY      900 ThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeuHisSerLeu 919
Db      2970 ACCCATGCCCCAGAGTAGGAGAGTACTTGAAGATGTCTCTGGAAGACCTGCATTCCTTG 3029
QY      920 AspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuLysCysAspAlaTyrMetCysMet 939
Db      3030 GACTCTCAGGAGAAATCCAAAGCTGTGCAGGAAGACTGCTTTGTGATGCATATATGTGCATG 3089
QY      940 TyrGlnSerProThrMetSerLeuTyrLys 949
Db      3090 TACCAGAGTCCCAACATGAGTTGTACAA 3119

RESULT 26
US-60-213-359-5981
; Sequence 5981, Application US/60213359
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lai, Preeti
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; TITLE OF INVENTION: Identified Thereby
; FILE REFERENCE: GX-0015 P
; CURRENT APPLICATION NUMBER: US/60/213,359
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 7924
; SOFTWARE: PERL Program
; SEQ ID NO 5981
; LENGTH: 6315
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 338326.5
; NAME/KEY: unsure
; LOCATION: 5942
; OTHER INFORMATION: a, t, c, g, or other
US-60-213-359-5981

Alignment Scores:
Pred. No.: 0 Length: 6315
Score: 4953.00 Matches: 944
Percent Similarity: 99.26% Conservative: 0
Best Local Similarity: 99.26% Mismatches: 2
Query Match: 98.39% Indels: 5
DB: 76 Gaps: 4

US-09-671-687A-3 (1-949) x US-60-213-359-5981 (1-6315)

QY      4 GlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIlePheTyrLeu 23
Db      270 GCGTTATGAGGCCAAGAAAGTCACTTCCACCTACTGGGAAGAGCGGATTTTTTACTTG 329
QY      24 LeuLeuGlnGluCysSerValThrAspLysGlnThrLysLeuLysValProLys 43
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Db      330 CTTCTTCAAGAAATGACGGTTTACAGACAAACACAAAGAGCTCCTTTAAAGTACCGAAG 389
QY      44 GlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIleProSerAla 63
Db      390 GGAAGTATAGACACAGTATATTCAAGATCGTTCTGTGGGGCATTTCAAGGATTCCTCTGCA 449
QY      64 LysGlyLysLysAenGlnIleGlyLeuLysIleLeuGluGlnProHisAlaValLeuPhe 83
Db      450 AAAGCAAGAAAAATCAGATTGGATTAAAAATTTAGAGCAACCTCATGACGTTCTCTTT 509
QY      84 ValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeuAlaIle 102
Db      510 GTTGATCAAAAGGATGTTGTAGACATAAATGAAAGTTTACAGAGATTACTTTTGGCAATT 569
QY      103 ThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnAtqLeuSerLysGlyLeu 122
Db      570 ACCAATTGTGAGGAGAGGTTGAGCTGTTTAAACAGAAACAGACTTAAGTAAAGCCCTC 629
QY      123 GlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGluLysPhePro 142
Db      630 CAAATAGACGTGGGCTGTCTGTGAAAGTACAGCTGAGATCTGGGGAAGAAAAATTTCT 689
QY      143 GlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGlyIlePhePhe 162
Db      690 GGAGTTGTAGCTTTCAGAGGACCTGTTAGCAGAGAGGACAGTCTCCGGAATATTCTTT 749
QY      163 GlyValGluLeuLeuGluGlyArgGlyGlnGlyPheThrAspGlyValTyrGlnGly 182
Db      750 GGAGTTGAAATTCGTGGGAAGAGGTCGTGGTCAAGGTTTCTCTGACGGGGTGTACCAAGGG 809
QY      183 LysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAspLysLeuGlu 201
Db      810 AAACAGCTTTTTCAGTGTGATGAGATTGTGGCGTGTGTTGTGTCATTGGACAAGCTAGAA 869
QY      202 LeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGlyAspThrMet 221
Db      870 CTCATAGAAGATGATGACATCTGCACTTGGAAAGTGATTACGCAAGTCTCTGGGACACAATG 929
QY      222 GlnValGluLeuProLeuGluIleAsnSerArgValSerLeuLysGlyGlyLthr 241
Db      930 CAGGTCGAATCTCTCTCTTGGAAATAAATCCAGAGTTTCTTTGAAGTTGGAGAAACA 989
QY      242 IleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSerLeuGlyTyr 261
Db      990 ATAGAATCTGGAACAGTTATTTCTGTGATGTTTTCAGGAAAGAAAGAAAGCTTAGATAT 1049
QY      262 PheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPheAspGlyVal 281
Db      1050 TTTGTTGGTGTGACATGGATAACCTTATTTGGCAACTGGGATGGAAGATTTGATGGAGTG 1109
QY      282 ---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsnAspIleIle 300
Db      1110 CAGCTTTGTAGTTTTCGCTGTGTTGAAAGTACATTTCTATTTCACATCAATGATATCATC 1169
QY      301 ProGluSerValThrGlnGluArgArgProLysLeuAlaPheMetSerArgGlyVal 320
Db      1170 CCAGAGAGTGTGACGAGGAAGAGGCCCTCCCAAACTTGCCTTTATGTCAAGAGGTGT 1229
QY      321 GlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThrSerAspPro 340
Db      1230 GGGGCAAAAGTTTCATCCAGTCATAATAAACCAAGGCTACAGGATCTACCTCAGACCT 1289
QY      341 GlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerValAspSerGln 359
Db      1290 GGAATAGAAACAGATCTGAATTTATTTATACCTTAAATGGGTCTTCTGTGTGACTCACAA 1349
QY      360 ProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAspProAlaLys 379
Db      1350 CCACAAATCCAAATCAAAAAATACATGTTGATGAAGTTGCAGAGACCCCTGCAAAA 1409
QY      380 SerLeuThrGluIleSerThrAspPheAspArgSerProProLeuGlnProProPro 399
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Db 1410 TCTCTTACAGATATCTACAGACTTTGACGGTTCTTCCACACACTCCAGCCTCCTCCT 1469  
QY ValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeuThrLysMet 419  
Db 1470 GTGAACCTCACTGACACCGAGACAGATTCCACTCTTTACCATTCAGTCTCACCCAGATG 1529  
QY 420 ProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGlnSerValMet 439  
Db 1530 CCCAATACCAATGGAAGTATTGGCCACAGTCCACTTTCTCTGTGAGCCAGTCTGTAATG 1589  
QY 440 GluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetProProGlyAsn 459  
Db 1590 GAAGAGCTAAACACTGCACCCGTCGAAGAGAGTCCACCTTGGCCATGSCCTCTCTGGGAAC 1649  
QY 460 SerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProProPheTyrGly 479  
Db 1650 TCACATGGTCTAGAAGTGGGCTCATTTGGCTGAAGTTAAGGAGAACCTCTCTCTCTATGGG 1709  
QY 480 ValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGlyLeuGluLeu 499  
Db 1710 GTAATCCGTGGATCGGTACGCCACCCAGGACTGAATGAAGTGTCTGCTGGACTGGAACGTG 1769  
QY 500 GluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyrPheThrCys 519  
Db 1770 GAAGATGAGTGTGCAGGCTGTACGGATGGAACCTTCAGAGGCACCTCGGTATTTTCACTGT 1829  
QY 520 AlaLeuLysAlaLeuPheValLysLeuLysSerCysArgProAspSerArgPheAla 539  
Db 1830 GCCCTGAAGAAGCGCTGTTTGTGAACCTGAAGAGCTGCAGGCGTGACTCTAGGTGTGCA 1889  
QY 540 SerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeu-AlaPheGlyGlyTy 559  
Db 1890 TCATTGACCGCGTTCATTCAGATTGAGGCTGTAACTCTTTAGGTATTTGGAGGCTA 1949  
QY 559 rLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGlyLeuGluIle 579  
Db 1950 CTTAAGTGAAGTAGTAGAAGAAAATCTCCACCAAAAATGMAAAAGAGCGTTGGAGAT 2009  
QY 579 eMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrIleuAspSerTh 599  
Db 2010 AATGATTGGGAAGAAGAGCGATCCAGGGTCAATTACAATTTCTTTGTTACTTAGACTCAAC 2069  
QY 599 rLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArgProLysG1 619  
Db 2070 CTTATTCTGCTTATTGCTTTAGTCTGTCTGGACACTGTGTTACTTAGACCAAGA 2129  
QY 619 uLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGluIleValas 639  
Db 2130 AAAGAACGATGTAGATATTATAGTGAACCCAGAGCTACTGAGGACAGAAATTTGTTAA 2189  
QY 639 nProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArgLysIleLe 659  
Db 2190 TCCTCTGAGAAATATATGATGTGTGTGTCACAAAAATTTATGAACTGAGGAAAAATACT 2249  
QY 659 uGluLysValGluAlaSerGlyPheThrSerGluGluLysAspProGluGluPheLe 679  
Db 2250 TGAAGAGTGGAGCTGCATCAGATTTACTCTGAAGAAAAAGATCCTGAGGAATTTCTT 2309  
QY 679 uAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArgSerAlaG1 699  
Db 2310 GAATATTCTTTTCATCATATTTTAAGGGTAGAACCTTTGCTAAAAATATAGATCAGCAGG 2369  
QY 699 yGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGluLysValG1 719  
Db 2370 TCAAAAGGTACAAGATTGTTACTTCTATCAAAATTTTATGMAAAAAATGAGAAAGTTGG 2429  
QY 719 yValProThrIleGlnLeuLeuGluTyrSerPheIleAsnSerAsnLeuLysPheAl 739  
Db 2430 CGTTCCCACAATTCAGCAGTGTGTAGAAATGGTCTTTTATCAACAGTAACCTGAAATTTGC 2489  
QY 739 aGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPheLysLeuPh 759  
Db 2490 AGAGGACCAATCATGCTCGATTATTTCAGATGCCCTCGATTGGAAAAAGACTTTAAACTATT 2549

QY 759 eLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAspThrProAr 779  
Db 2550 TAAAAAATTTTCTCTCTCGGAATTAATATAACAGATTTACTTTGAAGACACTCCCCAG 2609  
QY 779 gGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyrAspAspPr 799  
Db 2610 ACAGTCCGGATATGTGGAGGCTTGCAATGTATGAGTGTAGAGAATGCTACGACGATCC 2669  
QY 799 oAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGlnValHisLe 819  
Db 2670 GGACATCTCAGTCGAAAAATCAAGCAGTTTTGTAAAAACCTGCAACACTCAAGTCCACCT 2729  
QY 819 uHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAspLeuProAs 839  
Db 2730 TCATCCGAAGAGGCTGAATCATAAATATAACCCAGTGTCACTTCCCAAGAGCTTACCCGA 2789  
QY 839 pTTPAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAlaValLeuCy 859  
Db 2790 CTGGAGCTGGAGACACGGCTGCATCCCTTGGCAGAAATATGAGTATTATTTGCTGTCTCTG 2849  
QY 859 sIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSerAlaTrpLe 879  
Db 2850 CATAGAAACAAGCCACTATGTTGCTTTTGTGAAGTATGGGAAGGACGATTCTGCCTGGCT 2909  
QY 879 uPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIleProGlnVa 899  
Db 2910 CTTCTTTGACAGACTGCGCGATCGGATGGTGGTCAGAAATGGCTTCAACATTTCTTCAAGT 2969  
QY 899 lThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeuHisSerIle 919  
Db 2970 CACCCCATGCCAGAGTAGGAGAGTACTTGAAGATGTCTCTGGAAGACCTGCATTCCTT 3029  
QY 919 uAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyrMetCysMe 939  
Db 3030 GGACTCCAGGAGATCCAAAGGCTGTGCACGAAGACTGCTTTGTGATGCATATATGTGCAT 3089  
QY 939 tTyrGlnSerProThrMetSerLeuTyrLys 949  
Db 3090 GTACCAGAGTCCAACAATGATTTGTACAAA 3120

## RESULT 27

US-60-278-232-7384  
; Sequence 7384, Application US/60278232

; GENERAL INFORMATION:

; APPLICANT: Morris, MacDonald

; APPLICANT: Lal, Preeti

; APPLICANT: Diep, Dinh

; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using

; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide

; FILE REFERENCE: GX-0011 P

; CURRENT APPLICATION NUMBER: US/60/278,232

; CURRENT FILING DATE: 2001-03-30

; NUMBER OF SEQ ID NOS: 12,557

; SOFTWARE: PERL Program

; SEQ ID NO 7384

; LENGTH: 6316

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; OTHER INFORMATION: Incyte ID No: 338326.5

; NAME/KEY: unsure

; LOCATION: 5943

; OTHER INFORMATION: a, t, c, g, or other

US-60-278-232-7384

Alignment Scores:

Pred. No.: 0 Length: 6316

Score: 4953.00 Matches: 944

Percent Similarity: 99.26% Conservative: 0

Best Local Similarity: 99.26% Mismatches: 2

Query Match:	98.39%	Indels:	5
DB:	77	Gaps:	4
US-09-671-687A-3 (1-949) x US-60-278-232-7384 (1-6316)			
QY	4	GlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIlePheTyrLeu	23
DB	270	GGCTTATGGAGCCACAGAAAGTCACTTCACTCCCTACTGGGAGAGCGATTTTACTTG	329
QY	24	LeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLysValProLys	43
DB	330	CTTCTTCAAGATGCGACGCTTACAGACAAACAAACAAACAAAGCTCTTAAAGTACCGAAG	389
QY	44	GlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIleProSerAla	63
DB	390	GGAAATATAGGACAGTATATTCAGATCGTTCGTGTGGGCAATTCAGAGGATTCCTTCTGCA	449
QY	64	LysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnGlnProHisAlaValLeuPhe	83
DB	450	AAAGGACAGAAANTCAGATTGGATTAAATAATTCAGAGCAACTCATGCAATTCCTTT	509
QY	84	ValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeuAlaIle	102
DB	510	GTGTATGAAAAGGATCTGTAGAGATAAATGAAAAGTTACACAGATTACTTTTGGCAAT	569
QY	103	ThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSerLysGlyLeu	122
DB	570	ACCAATTTGTGAGGAGAGGTTACGCTCTTTAAATAACAGAAACAGACTAAGTAAAGGCTC	629
QY	123	GlnIleAspValClyCysProValLysValGlnLeuArgSerGlyGluGluLysPhePro	142
DB	630	CAAAATAGACGTGGGCTGTCTGTGAAAGTACAGCTGAGATCTGGGAAAGAAAATTTCT	689
QY	143	GlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGlyIlePhePhe	162
DB	690	GGAGTTGTACGTTTCAGAGACCCCTGTTAGCAGAGAGGACAGTCTCCGGAAATATTTCT	749
QY	163	GlyValGluLeuLeuGluGluArgGlyArgGlyGlnGlyPheThrAspGlyValTyrGlnGly	182
DB	750	CGAGTTGAATTCGTGGAAGAGGTCTGTGCTCAAGGTTTCACTGACGGGTGTACCAAGGG	809
QY	183	LysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAspLysLeuGlu	201
DB	810	AAACAGCTTTTTCAGTGTATGAAGATTGTGGCGTGTGTTGTCATTTGACAGCTAGAA	869
QY	202	LeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGlyAspThrMet	221
DB	870	CTCATAGAGATGATGACACTGATTTGGAAAGTATTACGAGGTCTCTGGGACACAATG	929
QY	222	GlnValGluLeuProLeuGluIleAsnSerArgValSerLeuLysGlyGlyGluThr	241
DB	930	CAGGTTCGAATCTCTCTTGGAAATAACTCCAGAGTTTCTTTGAAGTTGGAGAAACA	989
QY	242	IleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSerLeuGlyTyr	261
DB	990	ATAGAATCTGGAACAGTTATATCTGTGATGTTTTCGCCAGGAAAAGAAAGCTTAGGATAT	1049
QY	262	PheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPheAspGlyVal	281
DB	1050	TTTGTGTGTGGACATGGATAAACCTTATTGGCAACTTGGGATGGGAAGATTGTGAGGTG	1109
QY	282	---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsnAspIleIle	300
DB	1110	CAGCTTTGTAGTTTGGGTGTGTGAAAGTACAATTCATATGCACATCAATGATATCATC	1169
QY	301	ProGluSerValThrGlnGluArgArgProProLysLeuAlaPheMetSerArgGlyVal	320
DB	1170	CCAGAGAGTGTGACGACGAGAAAGGAGGCTCCCAAACTTGCCTTTATGTGCAAGAGTGT	1229
QY	321	GlyAspLysGlySerSerSerHisAsnLysProLysAlaThrGlySerThrSerAspPro	340
DB	1230	GGGACAAAGGTTTCACTCCAGTCAATAAACAAGGCTTACAGGATCTACCTCAGACCT	1289

QY	341	GlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerValAspSerGln	359
DB	1290	GGAAATAGAAACAGACTCTGAATTTATATACCTTAAATGGGTCTCTCTGTGACTCACAA	1349
QY	360	ProGlnSerLysSerLysAsnThrTyrTyrIleAspGluValAlaGluAspProAlaLys	379
DB	1350	CCACAAATCCAAATCAAAAATACATGTGTACATTTGATGAAGTTGCAGAGACCTTGCAAA	1409
QY	380	SerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGlnProProPro	399
DB	1410	TCTCTTACAGAGATATCTACAGACTTTTGACCGTTCTTCCACCACCACTCCAGCTCTCTCT	1469
QY	400	ValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeuThrLysMet	419
DB	1470	GTGAACCTCACTGACCCAGAGAACAGATTCACCTCTTTTACCATTTCAGTCTCCACCAAGATG	1529
QY	420	ProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGlnSerValMet	439
DB	1530	CCCATACCAATGGAAGTATTGGCCACAGTCCACTTCTGTGACGCCAGTCTGTGAATG	1589
QY	440	GluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetProProGlyAsn	459
DB	1590	GAAGAGCTAAACACTGACCCGTCACAGAGAGTCCACCCTTGGCCATGCTCTCTGGGAC	1649
QY	460	SerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProProPheTyrGly	479
DB	1650	TCACATGGTCTAGAAGTGGGCTCATTTGGCTGAAGTAAAGGAGAACCTCTCTTCTATGGG	1709
QY	480	ValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGlyLeuGluLeu	499
DB	1710	GTAAATCCGTTGGATCGGTGACCCAGCACTGAATGAAGTGTCTCGCTGGAGCTGGAACTG	1769
QY	500	GluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyrPheThrCys	519
DB	1770	GAAGATGAGTGTGCGAGCTGTACGGATGGAACTTTCAGAGGCACTCGGTATTTTACCTGT	1829
QY	520	AlaLeuLysLysAlaLeuPheValLysSerCysArgProAspSerArgPheAla	539
DB	1830	GCCTTGAAGAGGCGCTGTTTGTGAAACTGAAGAGCTGACGCCCTGACTCTAGGTTTGA	1889
QY	540	SerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeu-AlaPheGlyGlyTyr	559
DB	1890	TCATTCGAGCGGTTTCCAAATCAGATTGAGCGCTGTAACTCTTTAGGTATTTGGAGGCTA	1949
QY	559	rLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGlyLeuGluI	579
DB	1950	CTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAAATGGAAGAGGCTTGGAGAT	2009
QY	579	eMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeuAspSerTh	599
DB	2010	AATGATTTGGAGAGAGAAAGGCATCCAGGTCATTACAATCTTGTACTTTAGACTCAAC	2069
QY	599	rLeuPheCysLeuPheAlaPheSerValLeuAspThrValLeuLeuArgProLysGly	619
DB	2070	CTTATTCTGTCTTATTTGCTTTTAGTTCTGTCTTGACACCTGTGTACTTAGACCCAAAGA	2129
QY	619	ulysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGluIleValAs	639
DB	2130	AAAGAACGATGTAGAATATTTATAGTGAACCCCAAGAGCTACTGAGGACAGAAATTTGTAA	2189
QY	639	nProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArgLysIleLe	659
DB	2190	TCCTCTGAGATATATGGAATATGTGTGTCACAAAATATGAACTGAGGAAAAACT	2249
QY	659	uGluLysValGluAlaAspSerGlyPheThrSerGluGluLysAspProGluGluPheLe	679
DB	2250	TGAAGAGGTGGAGCTGCATCAGATTACTCTCTGAAGAAAAGATCCTCGGGAATCTT	2309
QY	679	uAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArgSerAlaGly	699
DB	2310	GAATATCTGTTTCATCATATTTTAAAGGGTAGAACCTTTTGTAAAAATAAGATCAGCAGG	2369
QY	699	yGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGluLysValGly	719

2370	Db		TCAAAGGTCACAGATTGTTACTTCTATCAAAATTTTATGGAATAAATGAGAAAGTTGG	2429
719	Qy	YValProThrIleGlnGlnLeuLeuGluTyrTpSerPheIleAsnSerAsnLeuLysPheAl	739	
2430	Db	CGTTCACCAAAATCAGCAGTTGTTAGAAATGGTCCTTTTATCAACAGTAACCTGAAATTTGC	2489	
739	Qy	aGluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPheLysLeuPh	759	
2490	Db	AGAGGCACCATCATGTCGTATTATTCAGATGCCTCGATTTGGAAAAAGACITTTAAACTATT	2549	
759	Qy	eLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAspThrProAr	779	
2550	Db	TAAAAAAATTTTCTCTCGAAATTAATAATAACAGATTACTTGAAGACACTCCCGAG	2609	
779	Qy	gGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyrAspAspPr	799	
2610	Db	ACATGTCGGCATATGTCGAGGGCTTGGCAATGTATGAGTGTAGAGATGCTACGACGATCC	2669	
799	Qy	oAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGlnValHisLe	819	
2670	Db	GGACATCTCAGCTGGAAAAATCAAGCAGTTTTTGTAAAACCTGCAACACTCAAGTCCACCT	2729	
819	Qy	uHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAspLeuProAs	839	
2730	Db	TCATCCGAAGAGCTGAATCATAAATATATACCCAGTGTCACTTCCCAAGACTTACCCGA	2789	
839	Qy	pTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAlaValLeuCy	859	
2790	Db	CTGGAGCTGGAGACACGGCTGCATCCCTTGCCAGAATATGAGGTTATTTGCTGTCTCTG	2849	
859	Qy	sIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSerAlaTrpLe	879	
2850	Db	CATAGAAAAAGCCACTATGTGTGTTTTGTGAAGTATGGGAAGACGATTCTGCCTGGCT	2909	
879	Qy	uPhePheAspSerMetalaspArgAspGlyGlyClnAsnGlyPheAsnIleProGlnVa	899	
2910	Db	CTTCTTTTGACAGCATGCCCGATCGGGATGGTGGTTCAGAAATGGCTTCAACATTCCTCAAGT	2969	
899	Qy	lThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeuHisSerLe	919	
2970	Db	CACCCCATGCCAGAGTAGGAGAGTACTTGAAGATGTTCTGGAGAAGCTGCAATTCCTT	3029	
919	Qy	uAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyrMetCysMe	939	
3030	Db	GGACTCCAGAGGAATCCAAAGGCTGTGCACGAAGACTGTTTGTGATGCATATATGTCAT	3089	
939	Qy	tTyrGlnSerProThrMetSerLeuTyrLys	949	
3090	Db	GTACCAGAGTCCAACAATGAGTTGTGACAAA	3120	

RESULT.T 28

RES001_28	US-09-786-797B-25	Qy	163	GlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyValTyrGlnGly	182
	; Sequence 25, Application US/09786797B				
	; GENERAL INFORMATION:	Db	749	GGAGTTGAATTGCTGGGAAGAGTCGTGGTCAAGGTTTCACTGACGGGGTGTACCAAGGG	808
	; APPLICANT: INCYTE PHARMACEUTICALS, INC.				
	; APPLICANT: LAL, Preeti	Qy	183	LysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAspLysLeuGlu	201
	; APPLICANT: TANG, Y. Tom				
	; APPLICANT: YUE, Henry	Db	809	AAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTTCCTGTCATTGGACAACCTAGAA	868
	; APPLICANT: HILLMAN, Jennifer L.				
	; APPLICANT: BANDMAN, Olga	Qy	202	LeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGlyAspThrMet	221
	; APPLICANT: CORLEY, Neil C.				
	; APPLICANT: GUEGLER, Karl J.	Db	869	CTCATGAAGATGATGACACTGTCATTGGAAAGTGATTACACAGGTCTCTGGGGACACAAATG	928
	; APPLICANT: PATTERSON, Chandra				
	; APPLICANT: AZIMZAI, Yalda	Qy	222	GlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGlyGlyGluThr	241
	; APPLICANT: BAUGHN, Mariah R.				
	; TITLE OF INVENTION: HUMAN CYTOSKELETON ASSOCIATED PROTEINS	Db	929	CAGTGCAACTTCTCTCTTTGGAAATAAACTCCACAGATTTCTTTGAAGTTGGAGAAACA	988
	; FILE REFERENCE: PF-0594 ECT				
	; CURRENT APPLICATION NUMBER: US/09/786,797B	Qy	242	IleGluSerGlyThrValIlePheCysAspValLeuPheGlyLysGluSerLeuGlyTyr	261
	; CURRENT FILING DATE: 2002-08-26				
	; PRIOR APPLICATION NUMBER: 09/156,470; unassigned; 60/131,321	Db	989	ATAGAATCTCGAAACAGTATATATCTCTGATGTTTTTGCAGGAAAGAAAGCTTATAGGATAT	1048
	; PRIOR FILING DATE: 1998-09-18; 1998-09-18; 1999-04-27				
	; NUMBER OF SEQ ID NOS: 32	Qy	262	PheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPheAspGlyVal	281

Db 1049 TTTGTTGGTGGACATGGATTAACCCCTATTGGCACTGGGATGGAAGATTGTGGAGTG 1108  
Qy 282 ---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsnAspIleIle 300  
Db 1109 CAGCTTTGTAGTTTGGTGTGTTGAAAGTACAATTCTATTGCACATCAATGATATCATC 1168  
Qy 301 ProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSerArgGlyVal 320  
Db 1169 CCAGAGAGTGTGACGAGGAAAGGAGGCCTCCCAAACTTGCCTTTATGTCAAGAGGTGTT 1228  
Qy 321 GlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThrSerAspPro 340  
Db 1229 GGGACAAAGGTTTCATCCAGTCATAATAAACCAAGGCTACAGGATCTACCTCAGACCCCT 1288  
Qy 341 GlyAsnArg---ArgSerGluLeuPheThrThrLeuAsnGlySerSerValAspSerGln 359  
Db 1289 GGAATAGAAACAGATCTGAATATTATTTATACCTTAATGGGTCTTCTGTGTGACTCAAA 1348  
Qy 360 ProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAspProAlaLys 379  
Db 1349 CCACAATCCAAATCAAAAATACATGTCATGTAATGAAAGTTCAGAAAGCCCTGCAAAA 1408  
Qy 380 SerLeuThrGluIleSerThrAspPheAspArgSerProProLeuGlnProProPro 399  
Db 1409 TCTCTTACAGAGATATCTACAGACTTTTGACCGTTCTTCCACCACACTCCAGCCCTCCT 1468  
Qy 400 ValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeuThrLysMet 419  
Db 1469 GTGAACCTACTGACCCAGAGAACAGATTTCACCTTTTACCATTCAGTCTACCAAGATG 1528  
Qy 420 ProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGlnSerValMet 439  
Db 1529 CCCAATACCAATGGAAGTATTGGCCACAGTCCACTTCTCTGTGACGCCAGTCTGTAATG 1588  
Qy 440 GluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetProProGlyAsn 459  
Db 1589 GAAGAGCTAAACACTGACCCGCTCCAAAGAGAGTCCACCTTTGGCCATGCTCTCTGGGAAC 1648  
Qy 460 SerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProProPheTyrGly 479  
Db 1649 TCACATGGTCTAGAAGTGGGCTCATTTGGCTGAAGTAAAGAGAACCTCTCTTTCTATGGG 1708  
Qy 480 ValIleArgTrpIleGlyGlnProProGlyLeuAsnGluValLeuAlaGlyLeuGluLeu 499  
Db 1709 GTAAATCCGTTGGATCGGTACGCCACACAGGACTGAAAGTGTCTCGTGGACTGGAACTG 1768  
Qy 500 GluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyrPheThrCys 519  
Db 1769 GAAGATGAGTGTGAGGCTGTACGGATGGAACCTTCAGAGGCACTCGGTATTTTACCTGT 1828  
Qy 520 AlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSerArgPheAla 539  
Db 1829 GCCCTGAAGAGGCGCTGTTGTGAAACTGAAGAGCTGCGAGGCTGACTCTAGGTTTGGCA 1888  
Qy 540 SerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPheGlyGlyTyr 559  
Db 1889 TCATTGAGCGGTTTTCCATCAGATTGAGCGCTGTAACCTTTTAGCATTTGGAGGCTAC 1948  
Qy 560 LeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGlyLeuGluIle 579  
Db 1949 TTAAGTGAAGTAGTAGAAGAAATACCTCCACCAAAAATGAAAAGAGAGGCTGGAGATA 2008  
Qy 580 MetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeuAspSerThr 599  
Db 2009 ATGATTGGGAAGAAAGAGCATCCAGGCTCAATTACAAATCTTGTACTTTAGACTCAACC 2068  
Qy 600 LeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArgProLysGlu 619  
Db 2069 TTAATCTGCTATTTGCTTTTAGTTCTGTTCTGAGCACTGTTGTACTTAGACCCCAAGAA 2128  
Qy 620 LysAsnAspValGluTyrTyrSerGluThrGlnLeuLeuArgThrGluIleValAsn 639

Db 2129 AAGAACGATGTAGAAATATTATAGTGAAACCCCAAGAGCTACTGAGGACAGAAATTGTAAAT 2188  
Qy 640 ProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArgLysIleLeu 659  
Db 2189 CCTCTGAGAAATATATGGATATGTGTGCCACAAAATATATGAACCTGAGGAAATATCTT 2248  
Qy 660 GluLysValGluAlaAlaSerGlyPheThrSerGluGluLysAspProGluGluPheLeu 679  
Db 2249 GAAAAGGTGGAGGCTGCATCAGGATTTACCTCTGAAGAAAAAGATCCTGAGGAATTTCTTG 2308  
Qy 680 AsnIleLeuPheHisHisIleLeuArgValGluProLeuLeuLysIleArgSerAlaGly 699  
Db 2309 AATATCTCTGTTTCATCATATTTTAAGGGTAGAACCTTTGCTAAAAATAAGATCAGCAGGT 2368  
Qy 700 GlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGluLysValGly 719  
Db 2369 CAAAAGGTACAGATTTGTACTTCTATCAATTTTTATGAAAAAATCGAGAAAGTTGGC 2428  
Qy 720 ValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeuLysPheAla 739  
Db 2429 GTTCCCACAATTCAGCAGTTGTAGATGGTCTTTTATCAACAGATAACCTGAAATTTGCA 2488  
Qy 740 GluAlaProSerCysLeuIleGlnMetProArgPheGlyLysAspPheLysLeuPhe 759  
Db 2489 GAGGACCATCATGTCTGATTATTAGATGCTCGATTTGGAAAAAGACTTTAAACTATTTT 2548  
Qy 760 LysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAspThrProArg 779  
Db 2549 AAAAAATTTTCTCTCTGGAATTAATAATATACAGATTTACTTGAAGACACTCCCAAG 2608  
Qy 780 GlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyrAspAspPro 799  
Db 2609 CAGTGCCGATATGTGGAGGCTTGTCAATGTATGATGTAGAGAATGCTACGACGATCCG 2668  
Qy 800 AspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGlnValHisLeu 819  
Db 2669 GACATCTCAGCTGAAAAAATCAAGCAGTTTGTGTAACCTGCAACACTCAAGTCCACCTT 2728  
Qy 820 HisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAspLeuProAsp 839  
Db 2729 CATCCGAAGAGCTGGAATCATATAATCAACCCAGTGTCACTTCCCAAGACTTACCCGAC 2788  
Qy 840 TrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAlaValLeuCys 859  
Db 2789 TGGGACTGGAGACACGCTGCATCCCTTGCAGAAATATGAGATTATTTGCTGTTCTCTGC 2848  
Qy 860 IleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSerAlaTrpLeu 879  
Db 2849 ATAGAAAACAGCCACTATGTTGCTTTGTGAAGTATGGGAAGGACGATTTGCTGCTGCTC 2908  
Qy 880 PhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIleProGlnVal 899  
Db 2909 TTTCTTTACAGCATGGCCGATCGGGATGGTGTGAGATGCTCTGGAAGAGACTGATTTCTTG 2968  
Qy 900 ThrProCysProGluValGlyGlyTyrLeuLysMetSerLeuGluAspLeuHisSerLeu 919  
Db 2969 ACCCATGCCAGAGTAGGAGAGTACTTGAAGATGCTCTGGAAGAGACTGATTTCTTG 3028  
Qy 920 AspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyrMetCysMet 939  
Db 3029 GACTCCAGGAGATCCCAAGGCTGTGCGAAGAGCTGCTTTGTGATGTCATATATGTGCAATG 3088  
Qy 940 TyrGlnSerProThrMetSerLeuTyrLys 949  
Db 3089 TACCAGAGTCCAAATCAGTGTGTACAAA 3118

## RESULT 29

US-10-921-707-25  
; Sequence 25, Application US/10921707  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE PHARMACEUTICALS, INC.  
; APPLICANT: LAL, Preeti  
; APPLICANT: TANG, Y. Tom

APPLICANT: YUE, Henry  
APPLICANT: HILLMAN, Jennifer L.  
APPLICANT: BANDMAN, Olga  
APPLICANT: CORLEY, Neil C.  
APPLICANT: GUEGLER, Karl J.  
APPLICANT: PATTERSON, Chandra  
APPLICANT: AZIMZAI, Yalda  
APPLICANT: BAUGHN, Mariah R.  
TITLE OF INVENTION: HUMAN CYTOSKELETON ASSOCIATED PROTEINS  
FILE REFERENCE: PF-0594 PCT  
CURRENT APPLICATION NUMBER: US/10/921,707  
CURRENT FILING DATE: 2004-08-19  
PRIOR APPLICATION NUMBER: US/09/786,797  
PRIOR FILING DATE: 2001-06-25  
PRIOR APPLICATION NUMBER: 09/156,470; unassigned: 60/131,321  
PRIOR FILING DATE: 1998-09-18; 1998-09-18; 1999-04-27  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PERL Program  
SEQ ID NO 25  
LENGTH: 4527  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No: 2363327  
US-10-921-707-25

Alignment Scores:  
Pred. No.: 0 Length: 4527  
Score: 4942.00 Matches: 944  
Percent Similarity: 99.37% Conservative: 0  
Best Local Similarity: 99.37% Mismatches: 2  
Query Match: 98.17% Indels: 5  
DB: 63 Gaps: 4

US-09-671-687A-3 (1-949) x US-10-921-707-25 (1-4527)

QY 4 GlyLeuTrpSerGlnGluValThrSerProTyrTrpGluGluArgIlePheTyrLeu 23  
Db 270 GGCCTTATGGAGCCAAAGAAAGTACATTCACCTTACTGGGAGAGCGGATTTTTTACTTG 329  
QY 24 LeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLysValProLys 43  
Db 330 CTTCTTCAAGATGCAGCGTTACAGACAAACAAACAAAGCTCTTTAAAGTACCGAA- 388  
QY 44 GlySerIleGlnTyrIleGlnAspArgSerValGlyHisSerArgIleProSerAla 63  
Db 389 GGAAGTATAGGACAGATATATCAAGATCGTTCTGTGGGGCATTCAAGGATTCTCTGCA 448  
QY 64 LysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAlaValLeuPhe 83  
Db 449 AAAGGCAAGAAAATCAGATTGGATTAAAAATTTAGAGCAACCTCATGAGTTCTCTTT 508  
QY 84 ValAspGlu---AspValValGluLeuAsnGluLysPheThrGluLeuLeuAlaIle 102  
Db 509 GTTGATGAAAGGATGTTGTAGAGATAATGAAAGTTTCAAGAGTTACTTTTGGCAATT 568  
QY 103 ThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSerLysGlyLeu 122  
Db 569 ACCAATTTGAGGAGAGGTTTCAGCTGTTTAAAAACAGAACAGACATAAGTAAAGGCGCT 628  
QY 123 GlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGluLysPhePro 142  
Db 629 CAAATAGACGTGGGCTGCTCTGTGAAAGTACAGCTGAGATCTGGGGAAGAAAATTTCT 688  
QY 143 GlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGlyIlePhePhe 162  
Db 689 GGAGTTGTACGCTTCAGAGGACCCCTGTTTACAGAGGACAGTCTCCGGAATATTCCT 748  
QY 163 GlyValGluLeuGluGluArgGlyGlnGlyPheThrAspGlyValTyrGlnGly 182  
Db 749 GGAGTTGATTTGCTGGAAGAGGTCGTGGTCAAGGTTTCACTGACGGGGTGTACCAAGGG 808

QY 183 LysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAspLysLeuGlu 201  
Db 809 AAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTGTGTCATTGCAAGCTAGAAA 868  
QY 202 LeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGlyAspThrMet 221  
Db 869 CTCATGAAGATGATGACATGCAATTTGGAAGTATGATACGCGAGGTCCTGGGACCAATG 928  
QY 222 GlnValGluLeuProLeuGluIleAsnSerArgValSerLeuLysGlyGlyGluThr 241  
Db 929 CAGTCTGAACCTTCTCTTTGGAATAAATCTCCAGAGTTTCTTTGAAGGTTGGAGAAC 988  
QY 242 IleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSerLeuGlyTyr 261  
Db 989 ATGAATCTGGAACAGTTATATTTCTGTGATGTTTTTCCAGGAAAGAAAGCTTAGGATAT 1048  
QY 262 PheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPheAspGlyVal 281  
Db 1049 TTTCTGTGTGGACATGGATAACCTTATTTGGCACTGGGATGGAAGATTTTGATGGAGTG 1108  
QY 282 ---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsnAspIleIle 300  
Db 1109 CAGCTTTGTAGTTTTGCGTGTGTTGAAAGTACAATTTATTGACATCAATGATATCATC 1168  
QY 301 ProGluSerValThrGlnGluArgProProLysLeuAlaPheMetSerArgGlyVal 320  
Db 1169 CCAGAGATGTGACGACGAGGAAGGAGGCTCTCCAACTTGCTTTATGTCAAGAGGTGT 1228  
QY 321 GlyAspLysGlySerSerSerHisAsnLysProLysAlaThrGlySerThrSerAspPro 340  
Db 1229 GGGGACAAAGGTTTCATCCAGTCATAATAAACAAGGCTACAGGATCTACCTCAGACCT 1288  
QY 341 GlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerValAspSerGln 359  
Db 1289 GGAATAGAAACAGATCTGAATTTATTTATACCTTAAATGGGTCTCTGTGTACTCACAA 1348  
QY 360 ProGlnSerLysSerLysAsnThrTriptyrIleAspGluValAlaGluAspProAlaLys 379  
Db 1349 CCACATCCAAATCAAAAATACATGTTACATGATGAAGTTGCAGAGACCTTCGCAAAA 1408  
QY 380 SerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGlnProProPro 399  
Db 1409 TCTCTTACAGAGATATCTACAGACTTTCAGCGCTTCTTACCACCACTTCAGGCTCTCTCT 1468  
QY 400 ValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeuThrLysMet 419  
Db 1469 GTGAACCTCACTGACCCAGCAAGACAGATTCCACTCTTTACCAATTCAGTCTCACCAGATG 1528  
QY 420 ProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGlnSerValMet 439  
Db 1529 CCCAATACCAATGGAGATTGTCAGCAGATCCACTTTTCTGTGTGAGCCAGTCTGTAAATG 1588  
QY 440 GluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetProProGlyAsn 459  
Db 1589 GAAGAGCTAAACACTGCACCCGCTCCAGAGAGATCCACCTTGGCCATGCTCTCTGGGAAC 1648  
QY 460 SerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProProPheTyrGly 479  
Db 1649 TCACATGCTCTAGAAGTGGGCTCATTTGGCTGAAGTTAAAGGAGAACCTCTTCTTATGGG 1708  
QY 480 ValIleArgTTrpIleGlyGlnProGlyLeuAsnGluValLeuAlaGlyLeuGluLeu 499  
Db 1709 GTAATCCGTTGGATCCGTCAGCCACAGACTGAATGAAGTCTGCTGTGAGCTGGAACTG 1768  
QY 500 GluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyrPheThrCys 519  
Db 1769 GAAGATGATGTGCGAGGCTGACGATGGAACCTTTCAGAGGCACTCGGTATTTACCTGT 1828  
QY 520 AlaLeuLysLysAlaLeuPheValLysLysSerCysArgProAspSerArgPheAla 539  
Db 1829 GCCCTGAAAGAGGCGCTGTTTGTGAACCTGAAGAGCTGCAGGCGCTGACTCTAGGTTTGA 1888  
QY 540 SerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPheGlyGlyTyr 559



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Db      1889 TCATTGAGCGGTTTCCAAATCAGATTGAGCGCTGTAACTCTTTAGCATTTGGAGGCTAC 1948
Qy      560 LeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGlyLeuGluIle 579
Db      1949 TTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAAAAGAGGCTTGGAGATA 2008
Qy      580 MetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeuAspSerThr 599
Db      2009 ATGATTGGGAAGAAGAGCATCCAGGGTCATTACAAATCTCTGTACTTAGACTCAACC 2068
Qy      600 LeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArgProLysGlu 619
Db      2069 TTATTCTGCTATTGCTTTTAGTTCTGTGTCGACACTGTGTACTTAGACCCAAAGAA 2128
Qy      620 LysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGluIleValAsn 639
Db      2129 AAGAAGATGTAGAAATATATAGTAAACCCAGAGCTACTGAGACAGAAATTTGTTAAT 2188
Qy      640 ProLeuArgIleTyrGlyTyrValCysAlaThrIysIleMetLysLysLeuArgLysIleLeu 659
Db      2189 CCTCTGAGAATATATGATATGTGTGCCACAAAATTTATGAACTGAGGAAATACTT 2248
Qy      660 GluLysValGluAlaIaSerGlyPheThrSerGluLysAspProGluGluPheLeu 679
Db      2249 GAAAAGGTGGAGCTGCATCAGGATTTACCTCTCAAGAAAAAGATCCTGAGGAATCTTG 2308
Qy      680 AsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArgSerAlaGly 699
Db      2309 AATATTCTGTTTCATCATATTTTAAGGGTAGAACCTTTGCTAAAAATPAAGATCAGCAGGT 2368
Qy      700 GlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGluLysValGly 719
Db      2369 CAAAAGGTACAGATTGTTACTTCTATCAATTTTATGAAAAAATGAGAAAGTTGGC 2428
Qy      720 ValProThrIleGlnGlnLeuLeuGluTyrSerPheIleAsnSerAsnLeuLysPheAla 739
Db      2429 GTTCCACCAATTGAGCAGTTGTTAGAAATGCTTTTATCAACAGTAACCTGAAATTTGCA 2488
Qy      740 GluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPheLysLeuPhe 759
Db      2489 GAGGCACCATCATGCTCGATTATTAGATGCTCGATTTGGAAGAGACTTTTAAACTATTT 2548
Qy      760 LysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAspThrProArg 779
Db      2549 AAAAAATTTTCTCTCTGGAATTAATATATACAGATTTACTTGAAGACATCTCCAGA 2608
Qy      780 GlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyrAspAspPro 799
Db      2609 CAGTGGCGGATATGTGGAGGCTTGCAATGTATGAGTGTAGAGAAATGCTACGACGATCCG 2668
Qy      800 AspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGlnValHisLeu 819
Db      2669 GACATCTCAGCTGGAATAATCAAGCAGTTTGTAAAACTGCAACACTCAAGTCCACCTT 2728
Qy      820 HisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAspLeuProAsp 839
Db      2729 CATCCGAAGAGGCTGAATCATAAATATAACCCAGTGTCACTTCCCAAGACTTACCCGAC 2788
Qy      840 TrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAlaValLeuCys 859
Db      2789 TGGGACTGGAGACACGGCTGCATCCCTGCCAGAAATAGAGTTATTGCTGTCTCTGC 2848
Qy      860 IleGluThrSerHisTyrValIaPheValLysTyrGlyLysAspSerAlaTrpLeu 879
Db      2849 ATAGAAACAAGCCACTATGCTGTTTGTGAAAGTATGGGAAGACGATTTGCTGCTGCTC 2908
Qy      880 PhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIleProGlnVal 899
Db      2909 TTTCTTTGACAGCATGGCCCATGGGATGGTGGTCAAGATGGCTTCAACATTTCTCAAGTC 2968
Qy      900 ThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeuHisSerLeu 919
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Db      2969 ACCCATGCCCAGAAAGTAGGAGAGTACTTGAAGATGTCTCTGGAAGACCTGCATTCCTTG 3028
Qy      920 AspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyrMetCysMet 939
Db      3029 GACTCCAGGAGATCCCAAGGCTGTGCACGAAGACTGCTTTGTGATGCATATATGTGATG 3088
Qy      940 TyrGlnSerProThrMetSerLeuTyrLys 949
Db      3089 TACCAGAGTCCCACAATGAGTTGTACAAA 3118

RESULT 30
US-60-131-321-21
; Sequence 21, Application US/60131321
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Lal, Preeti
; APPLICANT: Yue, Henry
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Azimzai, Valda
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN CYTOSKELETAL PROTEINS
; FILE REFERENCE: PF-0692 P
; CURRENT APPLICATION NUMBER: US/60/131.321
; CURRENT FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 21
; LENGTH: 4527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 2363327
US-60-131-321-21

Alignment Scores:
Pred. No.: 0 Length: 4527
Score: 0 942.00 Matches: 944
Percent Similarity: 99.37% Conservative: 0
Best Local Similarity: 99.37% Mismatches: 2
Query Match: 98.17% Indels: 5
DB: 75 Gaps: 4

US-09-671-687A-3 (1-949) x US-60-131-321-21 (1-4527)

Qy      4 GlyLeuTrpSerGlnGluLysValThrSerProTyrTrpGluGluArgIlePheTyrLeu 23
Db      270 GGCTTATGGAGCCCAAGAAAAAGTCACCTTACCTTACTGGGAAGAGCGGATTTTACTTTG 329
Qy      24 LeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLysValProLys 43
Db      330 CTTCTTCAAGAATGCAGCGTTTACAGACAAACAAACAAAAAGCTCTTAAAGTACCGAA- 388
Qy      44 GlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIleProSerAla 63
Db      389 GGAAGTATAGACAGATATATTCAAGATCGTTCTGTGGGCAATTCAAGGATTCCTTCTGCA 448
Qy      64 LysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGlnProHisAlaValLeuPhe 83
Db      449 AAAGGCCAAGAAAAATCAGATTGGATTAAAAATTTAGAGCAACCTCATGCAGTTCCTTTT 508
Qy      84 ValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeuAlaIle 102
Db      509 GTTGATGAAAAGGATGTTGTAGAGATAAATGAAAAGTTTACAGAGTTTACTTTTGGCAATT 568
Qy      103 ThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSerLysGlyLeu 122
Db      569 ACCAATTGTGAGGAGAGGTTTCAGGCTGTTTAAAAACAGAAACAGACTTAAGTAAAGGCTC 628
Qy      123 GlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluLysPhePro 142
Db      629 CAAATAGACGTGGCTGTCTCTGTGAAAGTACAGCTGAGATCTGGGGAAGAAAAATTTCTCT 688
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Db 2849 ATAGAAACAGCCACTATGTTGCTTTTGTGAGTATGGGAAGGACGATTCTGCCTGGCTC 2908  
Qy 880 PhePheAspSerMetAlaAspArgAspGlyGlnAsnGlyPheAsnIleProGlnVal 899  
Db 2909 TTCTTTGACAGCATGGCCGATCGGATGGTGGTGGATGGCTTCAACATTTCTTCAAGTC 2968  
Qy 900 ThrProCysProGluValGlyGluTyrluLeuLysMetSerLeuGluAspLeuHisSerLeu 919  
Db 2969 ACCCCATGCCAGAAAGTAGGAGAGTACTTGAAGATGCTCTGGGAAGACCTGCATTCCTTTG 3028  
Qy 920 AspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaIaTyrlMetCysMet 939  
Db 3029 GACTCAGGAGATCCAAAGCTGTGCAGAGACTGCTTTGTGATGCAATATATGTGCATG 3088  
Qy 940 TyrGlnSerProThrMetSerLeuTyrlLys 949  
Db 3089 TACCAGAGTCCAACATGAGTTTGTACAAA 3118  
RESULT 31  
US-60-172-360-22693  
; Sequence 22693, Application US/60172360  
; GENERAL INFORMATION:  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Lal, Preeti  
; APPLICANT: Diep, Dinh  
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using  
; FILE REFERENCE: Polynucleotide Sequence Databases, and Single Nucleotide Polymor  
; CURRENT APPLICATION NUMBER: US/60172,360  
; CURRENT FILING DATE: 1999-12-16  
; NUMBER OF SEQ ID NOS: 29838  
; SOFTWARE: PERL Program  
; SEQ ID NO 22693  
; LENGTH: 6315  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 338326.5  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 5942  
; OTHER INFORMATION: a, t, c, g, or other  
US-60-172-360-22693  
Alignment Scores:  
Pred. No.: 0 Length: 6315  
Score: 4916.00 Matches: 944  
Percent Similarity: 99.16% Conservative: 0  
Best Local Similarity: 99.16% Mismatches: 2  
Query Match: 97.66% Indels: 7  
DB: 75 Gaps: 4  
US-09-671-687A-3 (1-949) x US-60-172-360-22693 (1-6315)  
Qy 4 GlyLeuTrpSerGlnGluLysValThrSerProTyrlTrpGluGluArgIlePheTyrlLeu 23  
Db 270 GGCTTATGGAGCCAAAGAAAGTCACTTCACCTTACTGGGAAGCGGATTTTATCTTG 329  
Qy 24 LeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLysValProLys 43  
Db 330 CTCTTCAAGATGCAGCGTTACAGACAAACAAACAAAGCTCTTAAAGTACCAGAA- 388  
Qy 44 GlySerIleGlyInTyrlIleGlnAspArgSerValGlyHisSerArgIleProSerAla 63  
Db 389 GGAAGTATAGGACAGTATATTCAGATGCTGTGTGGGGCATTCAGGATTCCTTCTGCA 448  
Qy 64 LysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAlaValLeuPhe 83  
Db 449 AAAGGCAAGAAAAATCAGATTGGATTAAAAATTCTAGAGCAACCTCATGCGATTCTCTTT 508  
Qy 84 ValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeuLeuAlaIle 102

Db 509 GTTGATGAAAGGATGTTGTAGAGATAAATGAAAAGTTCAACAGAGTTACTTTTGGGCAAT 568  
Qy 102 eThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSerLysGlyLe 122  
Db 569 TACCAATTTGTGAGGAGAGTTTCAGCTCTTTAAAAAACAGAAACAGACATAAGTAAAGCCCT 628  
Qy 122 uGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGluLysPhePr 142  
Db 629 CCAATAGACGTGGCTGTCTGTGAAAGTACAGCTGAGATCTGGGGAGAAAAATTTCC 688  
Qy 142 oGlyValValArgPheArgGlyProLeuLeuAlaGluArgThrValSerGlyIlePhePh 162  
Db 689 TGGAGTTGTACGCTTCAGAGGACCCCTCTTAGCAGAGAGACAGTCTCCGGAATATTCTT 748  
Qy 162 eGlyValGluLeuLeuGluGlyArgGlyGlnGlyPheThrAspGlyValTyrlGlnG 182  
Db 749 TGGAGTTGAATTTGCTGGGAAGGTGCTGGTCAAGTTTCACTGACGGGTGTACCAAG 808  
Qy 182 YLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAspLysLeuGl 201  
Db 809 GAAACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTGTGTTCATTTGGCAACAGCTAGA 868  
Qy 201 uLeuIleGluAspAspThrAlaLeuGluSerAspTyrlAlaGlyProGlyAspThrMe 221  
Db 869 ACTCATGAAGATGATGACACTGCATTGGAAAGTATTACCGAGTCTCTGGGGACACAAT 928  
Qy 221 tGlnValGluLeuProLeuGluIleAsnSerArgValSerLeuLysGlyGlyLys 241  
Db 929 GCAGTGCMACTTCTCTTTGGAAATAAATCTCCAGAGTTTCTTTGAAGTTGGAGAAAC 988  
Qy 241 rIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSerLeuGlyTy 261  
Db 989 AATAGAATCTGGAACAGTTATATTCTGTGATGTTTTCAGGAAAAAGAAAGCTTAGGATA 1048  
Qy 261 rPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPheAspGlyVa 281  
Db 1049 TTTTGTGGTGTGACATGGATAACCTTATTTGGCAACTGGGATGGAAGATTGTGGAGT 1108  
Qy 281 l---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsnAspIleI 300  
Db 1109 GCAGCTTTGTAGTTTTCGCTGTGTGAAAGTACAAATCTATTGACATCAATGATATCAT 1168  
Qy 300 eProGluSerValThrGlnGluArgArgProProLysLeuAlaPheMetSerArgGlyVa 320  
Db 1169 CCCAGAGAGTGTGACGAGGAAAGAGGAGGCTCCCAACTTGCCTTTATGTCAAGAGGTGT 1228  
Qy 320 lGlyAspLysGlySerSerSerHisAsnLysProLysAlaThrGlySerThrSerAspPr 340  
Db 1229 TGGGGACAAAGGTTTCATCCAGTCAATAATAAACCAAGGCTACAGGATCTACCTCAGACC 1288  
Qy 340 oGlyAsnArg---ArgSerGluLeuPheTyrlThrLeuAsnGlySerSerValAspSerGl 359  
Db 1289 TGGAAATAGAAACAGATCTGAATTTATTTTATACCTTAATGGGTCTCTGTGTACTACA 1348  
Qy 359 nProGlnSerLysSerLysAsnThrTrpTyrlIleAspGluValAlaGluAspPro-AlaAl 379  
Db 1349 ACCAATATCCAAATCAAAAATAATACATGTATGATGAAAGTTGCAAGAGACCTTGGCA 1408  
Qy 379 ySerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGlnProProP 399  
Db 1409 AATCTCTTACAGAGATATCTACAGACTTGTACCGCTTCTTCCACCACCTCCAGGCTCTCT 1468  
Qy 399 roValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeuThrLysM 419  
Db 1469 CTGTGAATCTCACTGACCACCGAGAACAGATTCCTACTCTTTACCAATTCAGTCTCACAA 1528  
Qy 419 etProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGlnSerValM 439  
Db 1529 TGCCCAATACCAATGGAAGTATTGGCCACAGTCCACTTCTCTGTGACCCCATCTGTAA 1588  
Qy 439 etGluGluLeuAsnThrAlaProValGlnGluSerProProLeuAlaMetProProGlyA 459  
Db 1589 TGGNAGAGCTAAACACTGCGACCCCTCCNAGAGAGTCCACCCCTTGGCCATGCTCTCTGGGA 1648

Qy 459 snSerHisGlyLeuGluValGlySerLeuAlaGluValLysGluAsnProProPheTyrG 479  
Db 1649 ACTCACATGGTCTAGAAAGTGGCTCATTTGGCTGAAGTTAAGGAGAACCCCTCTTCTATG 1708  
Qy 479 lyValIleArgTTPilleGlyGlnProProGlyLeuAsnGluValLeuAlaGlyLeuGluL 499  
Db 1709 GGGTAATCCGTTGGATCGGTGAGCCAGCCAGGACTGAATGAAGTCTCGCTGAGCTGGAAC 1768  
Qy 499 euGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGlyThrArgTyrPheThrC 519  
Db 1769 TGAAGATGAGTGTGAGGCTGTACGATGGAACCTTCAGAGGCACTCGGTATTTTCACCT 1828  
Qy 519 ysaAlaLeuLysAlaLeuPheValLysLeuLysSerCysArgProAspSerArgPheA 539  
Db 1829 GTCCCTGAAGAGCGCTGTTTGTGAACCTGAAGAGCTGAGAGGCTCTAGGTGTTG 1888  
Qy 539 laSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSerLeuAlaPheGlyGlyT 559  
Db 1889 CATCATTTGACGCGGTTTCCAATCAGATTGAGCGCTGTAACCTTTTAGCATTTTGGAGCT 1948  
Qy 559 yrlLeuSerGluValValGluGluAsnThrProProLysMetGluLysGluGlyLeuGluI 579  
Db 1949 ACTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAATGGAAGAAAGAGGCTTTGGAGA 2008  
Qy 579 leMetIleGlyLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrLeuAspSerT 599  
Db 2009 TAATGATTTGGAGAGAGAGGCAATCCAGGCTCAATTAACATTTCTGTACTTAGACTCAA 2068  
Qy 599 hrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrValLeuLeuArgProLysG 619  
Db 2069 CCTTATTTCTGTTATTTGCTTTTAGTTCTGTTCTGGACACTGTTCTACTTAGACCCAAAG 2128  
Qy 619 luLysAsnAspValGluTyrTyrSerGluThrGlnGluLeuLeuArgThrGluIleVala 639  
Db 2129 AAAAGAACGATGTAGAATATTATAGTGAACCCAGAGCTACTCAGGACAGAAATTTGTTA 2188  
Qy 639 snProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMetLysLeuArgLysIleL 659  
Db 2189 ATCTCTCGAGAAATATGGATATGTGTGTGCCACAAAAATTTATGAACCTGAGGAAATAC 2248  
Qy 659 euGluLysValGluAlaSerGlyPheThrSerGluGluLysAspProGluGluPheL 679  
Db 2249 TTGAAGAGTGGAGCTGCATCAGATTACTCTGAAGAAAAGATCTCTGAGGAATCT 2308  
Qy 679 euAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleArgSerIaG 699  
Db 2309 TGAATATCTCTTCATCATATTTTAAGGGTAGAACCTTTGCTAAAAAATAAGATCAGCAG 2368  
Qy 699 lyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGluLysValG 719  
Db 2369 GTCAAAAGGTACAAAGATTGTACTTCTATCAAAATTTTATGGAAAAAATGAGAAAGTTG 2428  
Qy 719 lyValProThrIleGlnGlnLeuLeuGluTyrPheIleAsnSerAsnLeuLysPheA 739  
Db 2429 CGGTTCCACAAATTCAGCAGTTGTAGATGCTCTTTTATCAACAGTAACTCTGAATTTG 2488  
Qy 739 laGluAlaProSerCysLeuIleleGlnMetProArgPheGlyLysAspPheLysLeup 759  
Db 2489 CAGAGGCACCATCATGCTGATTTATTCAGATGCTCGATTTTGGAAAAAGACTTTAAACTAT 2548  
Qy 759 helysLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAspThrProA 779  
Db 2549 TTAATAAAATTTTCTCTCTGGAATTAATAATAACAGATTTTACTTTGAAGACACTCCCA 2608  
Qy 779 rgGlnCysArgIleCysGlyLeuAlaMetTyrGluCysArgGluCysTyrAspAsp 799  
Db 2609 GACAGTCCCGATATGTGGAGGCTTGCATGTATGAGTGTAGAGATGCTTACGACCATC 2668  
Qy 799 roAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGlnValHisL 819  
Db 2669 CGGACATCTCAGCTGGAAAAATCAAGCAGTTTGTGTAACCTGCAACACTCAAGTCCACC 2728

Qy 819 euHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAspLeuProA 839  
Db 2729 TTCAATCCGAGAGGCTGAATCATAAATATAAACCAGTGTCACTTCCCAAGACTTTACCCG 2788  
Qy 839 spTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAlaValLeuC 859  
Db 2789 ACTGGGACTGGAGACACGGCTGCATCCCTTCCAGAAATATGGAGTTATTTGCTGTCTCT 2848  
Qy 859 yslIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSerAlaTTP 879  
Db 2849 GCATAGAAACAAAGCCACTATGTTCTTTTGTGAAGATATGGGAAGGAGGATCTGCTGCGC 2908  
Qy 879 euPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIleProGlnV 899  
Db 2909 TCTTCTTTGACAGCATGCGCGATCGGATGTTGTTCAACATTCCTCAAG 2968  
Qy 899 alThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeuHisSerL 919  
Db 2969 TCACCCCATGCCAGAAAGTAGGAGACTTTGAAGATGCTCTCTGGAAGACCTGCAATTCCT 3028  
Qy 919 euAspSerArgArgIleGlnGlyCysAlaArgLeuLeuCysAspAlaTyrMetCysM 939  
Db 3029 TGGACTCCAGAGAAATCAAGGCTGTGCACGAAGACTGCTTTGTGATGCATATATGTGCA 3088  
Qy 939 etTyrGlnSerProThrMetSerLeuTyrLys 949  
Db 3089 TGTACCAAGACTCCAACTGATGTTGTACAAA 3120  
RESULT 32  
US-09-629-469A-18842  
; Sequence 18842, Application US/09629469A  
; GENERAL INFORMATION:  
; APPLICANT: OTA, TOSHIO  
; APPLICANT: ISOGAI, TAKAO  
; APPLICANT: NISHIKAWA, TETSUO  
; APPLICANT: HAYASHI, KOJI  
; APPLICANT: SAITO, KAORU  
; APPLICANT: YAMAMOTO, JUNICHI  
; APPLICANT: ISHII, SHIZUKO  
; APPLICANT: SUGIYAMA, TOMOYASU  
; APPLICANT: WAKAMATSU, AI  
; APPLICANT: NAGAI, KEIICHI  
; APPLICANT: OTSUKI, TETSUJI  
; TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH cDNA AND THEIR USE  
; FILE REFERENCE: 084335/0123  
; CURRENT APPLICATION NUMBER: US/09/629,469A  
; CURRENT FILING DATE: 2000-07-28  
; PRIOR APPLICATION NUMBER: JP 1999-248036  
; PRIOR FILING DATE: 1999-07-29  
; PRIOR APPLICATION NUMBER: JP 1999-300253  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: JP 2000-118776  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: JP 2000-183767  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: JP 2000-241899  
; PRIOR FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: 60/159,590  
; PRIOR FILING DATE: 1999-10-18  
; PRIOR APPLICATION NUMBER: 60/183,322  
; PRIOR FILING DATE: 2000-02-17  
; NUMBER OF SEQ ID NOS: 19025  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18842  
; LENGTH: 2845  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (452)..(2644)  
US-09-629-469A-18842  
Alignment Scores:

Pred. No.: 0 Length: 2845  
Score: 4601.00 Matches: 875  
Percent Similarity: 99.32% Conservative: 0  
Best Local Similarity: 99.32% Mismatches: 2  
Query Match: 91.40% Indels: 4  
DB: 28 Gaps: 4

US-09-671-687A-3 (1-949) x US-09-629-469A-18842 (1-2845)

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QY 92 AsnGluLysPheThrGluLeuLeuAlaIleThrAsnCysGluGluAArgPheSerLeu 111  
DB 62 AATGAAAGTTCACAGAGTTACTTTTGGCAATTACCAATTTGTGAGAGAGGTTTCAGCCTG 121

QY 112 PheLysAsnArgAsnArgLeuSerLysGlyLeuGlnIleAspValGlyCysProValLys 131  
DB 122 TTTTAAACAAAGAACAGACTAAGTAAGGGCTCCAAATAGACGTGGGCTGTCTGTGAAA 181

QY 132 ValGlnLeuArgSerGlyGluGluLysPheProGlyValValArgPheArgGlyProLeu 151  
DB 182 GTACAGCTGAGATCTGGGGAAGAAATTTCTGGAGTTGTACGCTTCAGAGGACCCCTG 241

QY 152 LeuAlaGluArgThrValSerGlyIlePhePheGlyValGluLeuLeuGluGlyArg 171  
DB 242 TTAGCAGAGAGGACAGTCTCCGGAATATTTCTTTGGAGTTGAAATTTGCTGGAAGAGGTCGT 301

QY 172 GlyGlnGlyPheThrAspGlyValTyrglnGlyLysGlnLeuPheGlnCysAspGluAsp 191  
DB 302 GGTCAAGGTTTCACTACGCGGGGTGTACCAAGGAAACAGCTTTTTCAGTGTGATGAAGAT 361

QY 192 CysGly---PheValAlaLeuAspLysLeuGluLeuIleGluAspAspThrAlaLeu 210  
DB 362 TGTGGCGTGTGTGCAATTTGGCAAGCTAGACTCATGAAGATGATGACACTGTGATG 421

QY 211 GluSerAspTyraAlaGlyProGlyAspThrMetGlnValGluLeuProProLeuGluile 230  
DB 422 GAAAGTGATTACCGAGTCTCTGGGACACAAATGAGTCAAGTCTCTCTTTGGAAATA 481

QY 231 AsnSerArgValSerLeuLysGlyGluThrIleGluSerGlyThrValIlePheCys 250  
DB 482 AACTCCAGAGTTTCTTTTGAAGGTTGGAGAAACAATAGAACTCTGGAACAGTTATATCTGT 541

QY 251 AspValLeuProGlyLysGluSerLeuGlyTyraPheValGlyValAspMetAspAsnPro 270  
DB 542 GATGTTTTCAGGAAAGAAAGCTTAGGATAATTTTGTGGTGTGGACATGGGATAACCCCT 601

QY 271 IleGlyAsnTrpAspGlyArgPheAspGlyVal---LeuCysSerPheAlaCysValGlu 289  
DB 602 ATTGGCAACTGGGATGGAGATTGTGAGTGCAGCTTTGTAGTTTGGCTGTGTGAA 661

QY 290 SerThrIleLeuLeuHisIleAsnAspIleIleProGluSerValThrGlnGluAArg 309  
DB 662 AGTACAAATCTATTGACATCAATGATATCATCCAGAGAGTGTGACGCGAGGAAAGAGG 721

QY 310 ProProLysLeuAlaPheMetSerArgGlyValGlyAspLysGlySerSerHisAsn 329  
DB 722 CCTCCCAAACTTGGCTTTATGTCAAGAGGTTGTTGGGACAAAGGTTTCATCCAGTCATAAT 781

QY 330 LysProLysAlaThrGlySerThrSerAspProGlyAsnArg---ArgSerGluLeuPhe 348  
DB 782 AAACCAAGGCTACAGGATCTACTCAGACCCCTGGAAATAGAAACAGATCTGAAATATTT 841

QY 349 TyrThrLeuAsnGlySerSerValAspSerGlnProGlnSerLysSerLysAsnThrTrp 368  
DB 842 TATACCTTAAATGGGTCTTCTGTGTGACTCACACCAATCCAAATCAAAAATATACATCG 901

QY 369 TyrIleAspGluValAlaGluAspProAlaLysSerLeuThrGluIleSerThrAspPhe 388  
DB 902 TACATTGATGAAGTTGAGAGAGACCCCTGCAAAATCTCTTACAGAGATATCTACAGACTTT 961

QY 389 AspArgSerSerProProLeuGlnProProValAsnSerLeuThrThrGluAsnArg 408  
DB 962 GACCGTTCTTTCACACCACTCCAGCTCTCTCTGTGAATCTCACTGACCAACCCAGAGACAGA 1021

QY 409 PheHisSerLeuProPheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHis 428  
DB 1022 TTCACACTTTTACCATTCAGTCTCACCAGATGCCAATACCAATGGAGATATTGGCCAC 1081

QY 429 SerProLeuSerLeuSerAlaGlnSerValMetGluGluLeuAsnThrAlaProValGln 448  
DB 1082 AGTCCACTTTCTCTGTCTGAGCCAGCTCTGTAATGGAGAGCTAAACACTGACCCCTCCAA 1141

QY 449 GluSerProProLeuAlaMetProGlyAsnSerHisGlyLeuGluValGlySerLeu 468  
DB 1142 GAGAGTCACCTTGGCCATGCTCTCTGGGAATCACAATGCTCTAGAAAGTGGCTCATTTG 1201

QY 469 AlaGluValLysGluAsnProPheTyrglyValIleArgTropIleGlyGlnProPro 488  
DB 1202 GCTGAAGTTTAAAGGAAACCTCTCTCTATGGGGTAATCCGTGGATCGGTCCGCCACCA 1261

QY 489 GlyLeuAsnGluValLeuAlaGlyLeuGluLeuGluAspGluCysAlaGlyCysThrAsp 508  
DB 1262 GGACTGAATGAGTCTGCTGGACTGGAATGGAAGATGAGTGTGCAAGGCTGTACGAT 1321

QY 509 GlyThrPheArgGlyThrArgTyraPheThrCysAlaLeuLysLysAlaLeuPheValLys 528  
DB 1322 GGAACCTTCAGAGCACTCGGTATTTCACTGTCTGCTGAAAGAGGCGCTGTTGTGAAA 1381

QY 529 LeuLysSerCysArgProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIle 548  
DB 1382 CTGAAGAGCTGCAAGGCTGACTCTAGGTTTGCATCATTTGCAAGCGGTTTCCAATCAGATT 1441

QY 549 GluArgCysAsnSerLeuAlaPheGlyGlyTyraLeuSerGluValValGluGluAsnThr 568  
DB 1442 GAGCGCTGTAACTCTTTAGCATTTGGAGGCTACTTAAAGTGAAGTAGTAGAAGAAATACT 1501

QY 569 ProProLysMetGluLysGluGlyLeuGluIleMetIleGlyLysLysLysGlyIleGln 588  
DB 1502 CCACCAAAATGGAAGAAAGGCTTCGAGATATATGATTCGGAAGAGAAAGGCATCCAG 1561

QY 589 GlyHisTyraAsnSerCysTyraLeuAspSerThrLeuPheCysLeuPheAlaPheSerSer 608  
DB 1562 GGTCAATTACAAATCTTGTACTTACCTCAACCTTATTTCTGCTTATTTGCTTTTAGTTCT 1621

QY 609 ValLeuAspThrValLeuLeuArgProLysGluLysAsnAspValGluTyraSerCys 628  
DB 1622 GTTCTGGACACTGTGTACTTGGACCCCAAGAAAGAACCGATGTAGAATATATTAGTGAA 1681

QY 629 ThrGlnGluLeuLeuArgThrGluIleValAsnProLeuArgIleTyraValCys 648  
DB 1682 ACCCAAGAGCTACTGAGGACAGAAATGTTAATCTCTGAGATATATGATATGTGTGT 1741

QY 649 AlaThrLysIleMetLysLeuArgLysIleLeuGluLysValGluAlaAlaSerGlyPhe 668  
DB 1742 GCCACAAAATATTAAGACTGAGGAAATATCTTGAAGAGGTGGAGGCTGCATCAGGATTT 1801

QY 669 ThrSerGluLysAspProGluGluPheLeuAsnIleLeuPheHisIleLeuArg 688  
DB 1802 ACCTCTGAAGAAAGATCTCTGAGGAATCTTGAATATTTCTGTTTCATCATATTTAAGG 1861

QY 689 ValGluProLeuLeuLysIleArgSerAlaGlyGlnLysValGlnAspCysTyraPheTyra 708  
DB 1862 GTAGAACCTTTGCTTAAATTAAGATCAGCAGGTCAAAGGTACAAAGATTGTTACTTCTAT 1921

QY 709 GlnIlePheMetGluLysAsnGluLysValGlyValProThrIleGlnGlnLeuLeuGlu 728  
DB 1922 CAAATTTTATGAAATAATGAGAAAGTTGGCGTTCACCAATTCAGCAGTGTGTAGAA 1981

QY 729 TrpSerPheIleAsnSerAsnLeuLysPheAlaGluAlaProSerCysLeuIleIleGln 748  
DB 1982 TGGTCTTTTATCAACAGTAACTGAAATTTGCAAGGACCATCATCTCTGATTTATTCAG 2041

QY 749 MetProArgPheGlyLysAspPheLysLeuPheLysLysIlePheProSerLeuGluLeu 768

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Db 2042 ATCCCTCGATTGGAAAGACTTTAAACTATTTAAAAAATTTTCTCTCTCGAATTA 2101
Qy 769 AsnIleThrAspLeuLeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAla 788
Db 2102 AATATAACAGATTACTTGAAGACACTCCAGACAGTCCCGGATATGTGGAGGCTTGCA 2161
Qy 789 MetTyrGluCysArgGluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGln 808
Db 2162 ATGTATGAGTGTAGAGATGCTACGACATCCGACATCTCAGCTGGAAATCAACGAG 2221
Qy 809 PheCysLysThrCysAsnThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyr 828
Db 2222 TTTTGTAAAAACCTGCACACTCAAGTCCACTTCATCCGAAGAGGCTGAATCAATAT 2281
Qy 829 AsnProValSerLeuProLysAspLeuProAspThrAspThrArgHisGlyCysIlePro 848
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Qy 849 CysGlnAsnMetGluLeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPhe 868
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Qy 869 ValLysTyrGlyLysAspSerAlaThrLeuPhePheAspSerMetAlaAspArgAsp 888
Db 2402 GTCAAGTATCGGAAGGACGATTTGCTGCTCTTCTTGCACAGCATGGCCGATCGGAT 2461
Qy 889 GlyGlyGlnAsnGlyPheAsnIleProGlnValThrProCysProGluValGlyLysTyr 908
Db 2462 GGTGGTCAAGTATGCTTCAACATTCCTCAAGTCAACCCATGCCAGAAAGTAGGAGATC 2521
Qy 909 LeuLysMetSerLeuGluAspLeuHisSerLeuAspSerArgArgIleGlnGlyCysAla 928
Db 2522 TTGAGATGCTCTGGAGACCTGCATCTCTTGGACTCCAGGAGATCCAGGCTGTGCA 2581
Qy 929 ArgArgLeuLeuCysAspAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyr 948
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Qy 949 Lys 949
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RESULT 33
US-10-917-503-18842
; Sequence 18842, Application US/10917503
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HAYASHI, KOJI
; APPLICANT: SAITO, KAORU
; APPLICANT: YAMAMOTO, JUNICHI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: WAKAMATSU, AI
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: OTSUKI, TETSUJI
; TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH cDNA AND THEIR USE
; FILE REFERENCE: 084335/0123
; CURRENT APPLICATION NUMBER: US/10/917,503
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US/09/629,469
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: JP 1999-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 1999-300253
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
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; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183,322
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 19025
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18842
; LENGTH: 2845
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (452)..(2644)
US-10-917-503-18842

Alignment Scores:
Pred. No.: 0 Length: 2845
Score: 4601.00 Matches: 875
Percent Similarity: 99.32% Conservative: 0
Best Local Similarity: 99.32% Mismatches: 2
Query Match: 91.40% Indels: 4
DB: 63 Gaps: 4

US-09-671-687A-3 (1-949) x US-10-917-503-18842 (1-2845)

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Qy 92 AsnGluLysPheThrGluLeuLeuAlaIleThrAsnCysGluGluArgPheSerLeu 111
Db 62 AATGAAAGTTACAGAGTTACTTTTGGCAATTACCAATTCTGAGGAGAGGTTACAGCTG 121
Qy 112 PheLysAsnArgAsnArgLeuSerLysGlyLeuGlnIleAspValGlyCysProValLys 131
Db 122 TTTAAAAACAGAAACAGACTAAGTAAAGGCTCCAAAATAGACGTGGGCTGTCTGTGAAA 181
Qy 132 ValGlnLeuArgSerGlyGluLysPheProGlyValValArgPheArgGlyProLeu 151
Db 182 GTACAGCTGAGATCTGGGGAAGAAAAATTTCTCGAGTTGTACGCTTCAGAGGACCCCTG 241
Qy 152 LeuAlaGluArgThrValSerGlyPhePheGlyValGluLeuLeuGluGlyArg 171
Db 242 TTAGCAGAGGACAGCTCTCCGGAATATTTCTTGGAGTTGAATGCTGAGAGAGAGTCTGT 301
Qy 172 GlyGlnGlyPheThrAspGlyValTyrGlnGlyLysGlnLeuPheGlnCysAspGluAsp 191
Db 302 GGTCAAGGTTTCACTGACGGGCTGTACCAAGGGAAACACAGCTTTTTCAGTGTGATCAAGAT 361
Qy 192 CysGly---PheValAlaLeuAspLysLeuIleGluAspAspThrAlaLeu 210
Db 362 TGTGGCGTGTGTTGTTGCAATGGACAAGCTAGAACTCATAGAAAGATGATGACACTGCATTG 421
Qy 211 GluSerAspTyrAlaGlyProGlyAspThrMetGlnValGluLeuProLeuGluIle 230
Db 422 GAAAGTGATTACGAGGCTCTGGGGACACAATGAGGTCGAACTTCCTCTTTGGAAATA 481
Qy 231 AsnSerArgValSerLeuLysGlyGluThrIleGluSerGlyThrValIlePheCys 250
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Qy 290 SerThrIleLeuLeuHisIleAsnAspIleIleProGluSerValThrGlnGluArgArg 309
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QY 349 TyrThrLeuAsnGlySerSerValAspSerGlnProGlnSerLysSerLysAsnThrTrp 368  
Db 842 TATACCTTAAATGGTCTTCTGTGACTCAACCAACCAATCCAAATCAAAATATACATGG 901  
QY 369 TyrIleAspGluValAlaGluAspProAlaLysSerIleThrGluIleSerThrAspPhe 388  
Db 902 TACATGTGATGAAGTGCAGAGACCTCGCAAAATCTCTTACAGAGATATCTACAGACTTT 961  
QY 389 AspArgSerSerProLeuGlnProProValAsnSerLeuThrGluAsnArg 408  
Db 962 GACCGTTCCTTACCAACACTCCAGCCCTCCTGTGAACCTACTGACCCAGAACAGAGA 1021  
QY 409 PheHisSerLeuProPheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHis 428  
Db 1022 TTCACCTCTTTACCACTTCAGTCTCACCAAGATGCCAATACCAATGGAAGTATGGCCAC 1081  
QY 429 SerProLeuSerLeuSerAlaGlnSerValMetGluGluLeuAsnThrAlaProValGln 448  
Db 1082 AGTCCACTTTCTCTGTGAGCCAGTCTGTGAATGGAAGAGCTAAACACTGCACCCGTCCTAA 1141  
QY 449 GluSerProProLeuAlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeu 468  
Db 1142 GAGAGTCCACCTTGGCCATGCTCTGCGAAGTCAACATGCTGTAGAAAGTGGGCTCATG 1201  
QY 469 AlaGluValLysGluAsnProProPheTyrGlyValIleArgTTPilleGlyGlnProPro 488  
Db 1202 GCTGAAGTTAAGAGAACCTCTCTTCTATGGGGTAATCCGTTGGATCGGTACGCCACCA 1261  
QY 489 GlyLeuAsnGluValLeuAlaGlyLeuGluLeuGluAspGluCysAlaGlyCysThrAsp 508  
Db 1262 GGACTGAATGAAGTCTGCTGAGCTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1321  
QY 509 GlyThrPheArgGlyThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLys 528  
Db 1322 GGAACCTTACAGAGCACTCGGTATTTTCCCTGTGCTGCTGGAAGGCGCTGTTGTGAAA 1381  
QY 529 LeuLysSerCysArgProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIle 548  
Db 1382 CTGAAGAGCTGCAGGCTGACTCTAGGTTTGCATCTATGTCAGCGGTTTCCAAATCAGATT 1441  
QY 549 GluArgCysAsnSerLeuAlaPheGlyGlyTyrLeuSerGluValValGluGluAsnThr 568  
Db 1442 GAGCGCTGTAACTCTTTAGCATTTGGAGGCTACTTAAGTGAAGTAGTAGAAGAAATACT 1501  
QY 569 ProProLysMetLysGluGlyLeuGluIleMetIleGlyLysLysGlyIleGln 588  
Db 1502 CCACCAAAATGAAAGAGGCTTGGAGATAATGATTGGGAAGAAAGGCAATCCAG 1561  
QY 589 GlyHisTyrAsnSerCysTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSer 608  
Db 1562 GGTCAATTAACATTTCTGTACTTAGACTCAACCTTATCTGCTTATTTGCTTTTAGTTCT 1621  
QY 609 ValLeuAspThrValLeuLeuArgProLysGluLysAsnAspValGluTyrTyrSerGlu 628  
Db 1622 GTTCTGGACACTGTGTACTTGGACCCCAAGAAAGAACGATGTAGAAATATATAGTGAA 1681  
QY 629 ThrGlnGluLeuLeuArgThrGluIleValAsnProLeuArgIleTyrGlyTyrValCys 648  
Db 1682 ACCCAAGAGCTACTGAGGACAGAAATGTTAATCTCTGAGATATATGATATGTGT 1741  
QY 649 AlaThrLysIleMetLysLeuArgLysIleLeuGluLysValGluAlaLalaSerGlyPhe 668  
Db 1742 GCCACAAAAATATGAAACTGAGGAAAAATCTTGAAGAGGAGGAGGCTGCATCAGGATTT 1801

QY 669 ThrSerGluGluLysAspProGluPheLeuAsnIleLeuPheHisIleLeuArg 688  
Db 1802 ACCTCTGAAGAAAAAGATCCTGAGGAATTTCTGAATATTTCTGTTTCATATATTTAAGG 1861  
QY 689 ValGluProLeuLeuLysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyr 708  
Db 1862 GTAGAACCTTTGCTTAAATAANTAGATCAGCAGGTCAAAAGGTCAAGATTGTTACTTCTAT 1921  
QY 709 GlnIlePheMetGluLysAsnGluLysValGlyValProThrIleGlnGlnLeuGlu 728  
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QY 729 TrpSerPheIleAsnSerAsnLeuLysPheAlaGluAlaProSerCysLeuIleGln 748  
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QY 749 MetProArgPheGlyLysAspPheLysLeuPheLysIlePheProSerLeuGluLeu 768  
Db 2042 ATGCTCGATTGGAAAGACTTTTAAACTATTTAAAAAATTTTCTCTCTGGAATTA 2101  
QY 769 AsnIleThrAspLeuLeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAla 788  
Db 2102 AATATAACAGATTACTTTGAAGACACTCCAGACAGTCCCGGATATGTGGAGGGCTGCA 2161  
QY 789 MetTyrGluCysArgGluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGln 808  
Db 2162 ATGTATGAGTGTAGAGATGCTACAGCATCCGACATCTCAGCTGGAATAATCAAGCAG 2221  
QY 809 PheCysLysThrCysAsnThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyr 828  
Db 2222 TTTTGTAAAACTTCCACACTCAAGTCCACTTTCATCCGAAGAGGCTGAATCATAAATAT 2281  
QY 829 AsnProValSerLeuProLysAspLeuProAspTrpAspTrpArgHisGlyCysIlePro 848  
Db 2282 AACCCAGTGTCACTTCCAAAGACTTTACCCGACTGGGACTGGAGACACGGCTGCATCCCT 2341  
QY 849 CysGlnAsnMetGluLeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPhe 868  
Db 2342 TGCCAGAAATATGGAGTTATTTGCTGTTCTCTGTCATAGAAACAAGCCACTATGTTGCTTT 2401  
QY 869 ValLysTyrGlyLysAspAspSerAlaTrpLeuPhePheAspSerMetAlaAspArgAsp 888  
Db 2402 GTGAAGTATGGGAAGGACGATTTCTGCTGGCTCTTTTGTGACAGCATGCCGATCGGAT 2461  
QY 889 GlyGlyGlnAsnGlyPheAsnIleProGlnValThrProCysProGluValGlyGluTyr 908  
Db 2462 GGTGGTCAAGATGGCTTCAACATTTCTCAAGTACCCTCATGCCAGAAAGTAGGAGATAC 2521  
QY 909 LeuLysMetSerLeuGluAspLeuHisSerLeuAspSerArgArgIleGlnGlyCysAla 928  
Db 2522 TTGAAGATGTTCTTGGGAAGACCTGCATTTCTTGGACTCCAGAGAAATCCAGGCTGTGCA 2581  
QY 929 ArgArgLeuLeuCysAspAlaTyrMetCysMetTyrGlnSerProThrMetSerLeuTyr 948  
Db 2582 CGAAGACTGCTTTGTGATGCATATATGTGATGTACAGAGTCCCAACAATGAGTTGTGATAC 2641  
QY 949 Lys 949  
Db 2642 AAA 2644

Search completed: January 16, 2006, 14:11:35

Job time : 10028 secs







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Db      2857 GTTCTCTGCATAGAAACCAACCCACTATGTTGCTTTTGTGAGATATGGGAAGGACGATTCT 2916
QY      877 AlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGlyPheAsnIle 896
Db      2917 GCCTGGCTCTTCTTTCACAGCATGGCCGATGGGATGGTGTGAGATGCTTCAACATT 2976
QY      897 ProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeuGluAspLeu 916
Db      2977 CCTCAAGTCACCCCATGCCAGAAAGTAGGAGAGTACTTGAAGATGCTCTGGAAGACCTG 3036
QY      917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936
Db      3037 CATTCTCTGGACCTCAGAGGAATCCAAAGCTGTGCGAAGACTGCTTTGTGATGCATAT 3096
QY      937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db      3097 ATGTGCATGTACCAGAGTCCAAACAATGAGTTGTACAAA 3135

RESULT 2
US-60-751-420-3015
; Sequence 3015, Application US/60751420
; GENERAL INFORMATION:
; APPLICANT: Raelson, John Verner
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Bradley, Walter Edward
; APPLICANT: Paquin, Bruno
; APPLICANT: Fournier, Helene
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
; APPLICANT: Debrus, Sophie
; APPLICANT: Van Eerdewegh, Paul
; APPLICANT: Little, Randall David
; APPLICANT: Keith, Tim
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: GeneMap of the human genes associated with Crohn's disease
; FILE REFERENCE: GEN-011/00US
; CURRENT APPLICATION NUMBER: US/60/751,420
; CURRENT FILING DATE: 2005-12-19
; NUMBER OF SEQ ID NOS: 27266
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3015
; LENGTH: 5371
; TYPE: DNA
; ORGANISM: Homosapiens
US-60-751-420-3015

Alignment Scores:
Pred. No.: 0 Length: 5371
Score: 4971.50 Matches: 948
Percent Similarity: 99.16% Conservative: 0
Best Local Similarity: 99.16% Mismatches: 1
Query Match: 98.76% Indels: 7
DB: 10 Gaps: 5

US-09-671-687A-3 (1-949) x US-60-751-420-3015 (1-5371)

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Job time : 1011 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame\_plus p2n model

Run on: January 15, 2006, 21:47:59 ; Search time 42759 Seconds  
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Post-processing: Minimum Match 90%  
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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1  
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DEFINITION Sequence 95 from Patent WO2004058805.  
ACCESSION CQ834224  
VERSION CQ834224.1 GI:50833761  
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SOURCE  
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Hominidae; Homo.  
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Matsuda, A. and Yoneta, S.  
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Patent: WO 2004058805-A 95 15-JUL-2004;  
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ORIGIN

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Best Local Similarity: 99.48% Mismatches: 1  
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DB: 6 Gaps: 4

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VERSION BC012342.1 GI:15214433  
KEYWORDS MGC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 3540)  
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettner,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A.C., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,J.S., Krzywinski,W.I., Skalska,U., Smallus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
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2 (bases 1 to 3540)  
Strausberg,R.  
Direct Submission  
Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: http://mgc.nci.nih.gov  
Contact: MGC help desk  
Email: cgapbe-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
info@bcgsc.bc.ca  
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Series: IRAL Plate: 29 Row: c Column: 5  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14165257.  
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US-09-671-687A-3 (1-949) x BC012342 (1-3540)

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Hominidae; Homo.  
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REFERENCE  
AUTHORS Abbas,A.; Clark,H.; Ouyang,W.; Williams,M.P.; Wood,W.I. and Wu,T.D.  
TITLE Compositions and methods for the treatment of immune related diseases  
JOURNAL Patent: WO 2005016962-A 3672 24-FEB-2005;  
Genentech, Inc. (US)  
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Qy	377	ProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerProProLeuGln	396
Db	1587	CCTGCAAAATCTTTACAGATATCTACAGACTTTGACCGTTCTTACCAACCACTCCAG	1646
Qy	397	ProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerLeu	416
Db	1647	CCTCCTCTGTGAATCACTGACCCAGACCAACAGATTCCCACTCTTTACCAATTCAGTCTC	1706
Qy	417	ThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGln	436
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Qy	477	PheTyrGlyValIleArgTrpIleGlyClnProProGlyLeuAsnGluValLeuAlaGly	496
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 DEFINITION Sequence 3672 from Patent WO2005019258.  
 ACCESSION CS043118  
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 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.

REFERENCE 1  
 AUTHORS Abbas, A., Clark, H., Ouyang, W., Williams, P. M., Wood, W. I. and Wu, T. D.  
 TITLE Compositions and methods for the treatment of immune related diseases  
 JOURNAL Patent: WO 2005019258-A 3672 03-MAR-2005;  
 Genentech, Inc. (US)

FEATURES  
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US-09-671-687A-3 (1-949) x CS043118 (1-5414)

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## RESULT 5

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DEFINITION Homo sapiens mRNA for KIAA0849 protein, partial cds.

ACCESSION AB020656

VERSION AB020656.2 GI:14133220

KEYWORDS Homo sapiens (human)

SOURCE ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (sites)

Nagase, T., Ishikawa, K., Suyama, M., Kikuno, R., Hiroseawa, M.,

Miyajima, N., Tanaka, A., Kotani, H., Nomura, N. and Ohara, O.

Prediction of the coding sequences of unidentified human genes.

XII. The complete sequences of 100 new cDNA clones from brain which

code for large proteins in vitro

DNA Res. 5 (6), 355-364 (1998)

10048485

2 (bases 1 to 5414)

Ohara, O., Suyama, M., Kikuno, R., Nagase, T. and Ishikawa, K.

Direct Submission

Submitted (02-DEC-1998) Osamu Ohara, Kazusa DNA Research Institute,

Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba

292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,

Fax:+81-438-52-3914)

On May 17, 2001 this sequence version replaced gi:4240186.

Location/Qualifiers

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US-09-671-687A-3 (1-949) x AB020656 (1-5414)

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CQ834222

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ACCESSION CQ834222  
VERSION CQ834222.1 GI:50833759  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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Hominidae; Homo.  
REFERENCE 1  
AUTHORS Matsuda, A. and Yoneta, S.  
TITLE T cell activating gene  
JOURNAL Patent: WO 2004058805-A 93 15-JUL-2004;  
Asahi Kasei Pharma Corporation (JP)  
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REFERENCE
AUTHORS    Bignell,G.R., Brown,C., Biggs,P.J., Lakhani,S.R., Jones,C.,
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TITLE      Identification of the familial cyldromatosis tumour-suppressor
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JOURNAL    Nat. Genet. 25 (2), 160-165 (2000)
PUBMED    10835629
REFERENCE  2 (bases 1 to 5371)
AUTHORS    Stratton,M.R.
TITLE      Direct Submission
JOURNAL    Submitted (29-NOV-1999) Stratton M.R., Cancer Genetics, Institute
            of Cancer Research, 15 Cotswold Rd., Sutton, Surrey, SM2 5NG.,
            UNITED KINGDOM

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ORIGIN
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DB:              8      Gaps:      5

US-09-671-687A-3 (1-949) x HSA250014 (1-5371)

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QY      21   PheTyrLeuLeuLeuGlnGluCysSerValThrAspLysGlnThrGlnLysLeuLeuLys 40
Db      452  TTTTACTTGTCTTCTTCAAGAAATGCGCGTTACACAAACAAACAAACAAAGCTCTCTAAA 511
QY      41   ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
Db      512  GTACCGAAGGGAAGTATAGGACAGTATATCAAGATCGTCTGTGGGCGATTCAAGGATT 571
QY      61   ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuIlyLeuGluGlnProHisAla 80
Db      572  CCTTCTGCAAAAGGCAAGAAAAATCAGATTGGATTAATAAATCTTAGAGCAACCTCATGCA 631
QY      81   ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99
Db      632  GTTCTCTTTTGTGATGAAAAGGATGTTGTAGAGATAAATGAAAAGTTTCACAGAGTACTT 691
QY      100  LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnArgAsnArgLeuSer 119
Db      692  TTGGCAATTAACCAATTGTGAGAGAGAGGTTTACCTGTTTTAAAAACAGAAACAGACTAAGT 751
QY      120  LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
Db      752  AAAGGCTCCAAATAGACGTGGGCTGTCTGTGAAAGTACAGCTGAGATCTGGGGAAGAA 811
QY      140  LysPheProGlyValValArgPheArgProLeuLeuAlaGluArgThrValSerGly 159
Db      812  AAATTTCTCGAGTGTGTACGCTTCAGAGGACCCCTGTTTAGCAGAGAGGACAGTCTCCCGA 871
QY      160  IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal 179
Db      872  ATATTCTTGGAGTTGAATTGCTGGAAGAAGGTCTGTGCTCAAGGTTTTCACCTACCGGGTG 931
QY      180  TyrGlnGlyLysGlnLeuPheGlnCysAspGluAspCysGly---PheValAlaLeuAsp 198
Db      932  TACCAAGGGAACACAGCTTTTTCAGTGTGATGAAGATTGTGGCGTCTTTGTTGTCATTGGAC 991
QY      199  LysLeuGluLeuIleGluAspAspThrAlaLeuGluSerAspTyrAlaGlyProGly 218

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Db	992		AGCTAGAACTCTAGAGATGATGACCTGCAATTTGGAAAGTGATTACCGAGGTCTCTGGG	1051
QY	219		AspThrMetGlnValGluLeuProProLeuGluIleAAsnSerArgValSerLeuLysGly	238
Db	1052		GACACAATGCAGTGCAGCTTCTCTCTTTGGAAATAAATCCAGAGTTCTTCTGAGGTT	1111
QY	239		GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer	258
Db	1112		GGAGAAACAATAAGAACTCGAAACAGTTATATCTGTGATGTTTGGCCAGGAAAGAAGC	1171
QY	259		LeuGlyTyrPheValGlyValAspMetAspAspProIleGlyAsnTrpAspGlyArgPhe	278
Db	1172		TTAGGATAATTTGTTGGTGGGACATGGATAACCTATTGGCAACTGGGATGGAAGATT	1231
QY	279		AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn	297
Db	1232		GATGGAGTCAGCTTTGTAGTTTGGTGTGTGTTGAAAGTACAAATTTCTATTGCATCAAT	1291
QY	298		AspIleIlePro-----GluSerValThrGlnGluArgProProLysLeuAla	314
Db	1292		GATATCATCCAGCTTTATCAGAGAGTGTGACGCGAGAAAGGAGGCTCCCAAACTTGCC	1351
QY	315		PheMetSerArgGlyValGlyAspLysGlySerSerSerHisAsnLysProLysAlaThr	334
Db	1352		TTTATGTCAAGAGGTGTGGGCAAGGTTCATCCAGTCATATAAACCACAAAGGCTACA	1411
QY	335		GlySerThrSerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGly	353
Db	1412		GGATCTACCTCAGACCTCGAATAAGAAACAGATCTGAATATTTTATACCTTAATATGGG	1471
QY	354		SerSerValAspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluVal	373
Db	1472		TCTTCTGTTGACTCACACACCAATCCAAATCAAATAATACATGTTGATGATGAGTT	1531
QY	374		AlaGluAspProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerPro	393
Db	1532		GCAGAAGACCCCTGCAAAATCTCTTACAGAGATATCTACAGACTTTGACCGTTCTCACCA	1591
QY	394		ProLeuGlnProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuPro	413
Db	1592		CCACTCCAGCTCTCTCTGTGAACCTCACTGACACCCGAGAACAGATTCACACTCTTTACCA	1651
QY	414		PheSerLeuThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeu	433
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Db	1712		TCAGGCCAGTCTGTAATGGAAGAGCTAAACACTGCCACCCGTCACAGAGAGTCCACCCCTTG	1771
QY	454		AlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValLysGlu	473
Db	1772		GCCATGCCCTCTCTGGAACTCACATGCTCTAGAAAGTGGGCTCATTTGGCTGAAAGTAAAGGAG	1831
QY	474		AsnProProPheTyrGlyValIleArgTrpIleGlyGlnProProGlyLeuAsnGluVal	493
Db	1832		AAACCTCTCTTTCTATGGGTAATTCCTGTGATCGGTGACCCACAGACTGGAATGAAGTG	1891
QY	494		LeuAlaGlyLeuLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGly	513
Db	1892		CTCGCTGGACTGGAACCTGGAAGATGAGTGTGCAGGCTGTACGGATGGAACCTTCAGAGGC	1951
QY	514		ThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArg	533
Db	1952		ACTCGTATTTACCTGTGCCCTGGAAGAAGGCGCTGTTGTGAAACTGAAGAGCTGCAGG	2011
QY	534		ProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSer	553
Db	2012		CCTGACTCTAGGTTTGTGCATCATTTGCAGCCGGTTTCCAATCAGATTGAGCGCTGTAACTCT	2071
QY	554		LeuAlaPheGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGlu	573
Db				
Db	2072		TTAGCATTTGGAGCTACTTAAGTGAAGTAGTAGAAGAAATACTCCACCAAAAATGGAA	2131
QY	574		LysGluGlyLeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSer	593
Db	2132		AAAGAAGGCTTGGAGATAATGATTGGGAAGAAAGAGGCATCCAGGGTCATTACAAATCT	2191
QY	594		CysTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSerValLeuAspThrVal	613
Db	2192		TGTTACTTAGACTCAACCTTATTCTGCTTATTTCTCTTTAGTTCTGTCTCTGGACACTGG	2251
QY	614		LeuLeuArgProLysGluLysAsnAspValGluLysTyrSerGluThrGlnGluLeuLeu	633
Db	2252		TTACTTAGACCCCAAGAAAGAACGATGAGAAATATATAGTAGAAACCAAGAGCTACTG	2311
QY	634		ArgThrGluIleValAsnProLeuArgIleTyrGlyTyrValCysAlaThrLysIleMet	653
Db	2312		AGGACAGAAATTTGTAATCCTCTGAGAAATATATGATATGTTGTGTGCCACAAAATATG	2371
QY	654		LysLeuArgLysIleLeuGluLysValGluAlaAlaSerGlyPheThrSerGluGluLys	673
Db	2372		AAACTGAGGAAATACTTGAAGAGGTGGAGCTGCATCAGGATTTTACCTCTGAAAGAAA	2431
QY	674		AspProGluGluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeu	693
Db	2432		GATCCTGAGGAATTTCTTGAATATTTCTGTTTCATCATATTTTAAAGGTAGAACCTTTGCTA	2491
QY	694		LysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGlu	713
Db	2492		AAATTAAGATCAGCAGGTCAAAGGTACAAGATTGTTACTTCTATCAAAATTTTATGGAA	2551
QY	714		LysAsnGluLysValGlyValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsn	733
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QY	734		SerAsnLeuLysPheAlaGluAlaProSerCysLeuIleIleGlnMetProArgPheGly	753
Db	2612		AGTAACCTGAAATTTGAGAGGACCATCATGTCGTGATTATTTCAGATGCCCTCGATTTGGA	2671
QY	754		LysAspPheLysLeuPheLysLysIlePheProSerLeuGluLeuAsnIleThrAspLeu	773
Db	2672		AAAGACTTTAAACTATTTTAAAAAAATTTTCTCTCTGGAATTAATAATACAGATTTA	2731
QY	774		LeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArg	793
Db	2732		CTTGAAGACACTCCAGACAGTGCCTGATATGTGGAGGCTTGCATATGATAGTGTAGTA	2791
QY	794		GluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCys	813
Db	2792		GAATGCTACGACGATCCGACATCTCAGCTGGAATAATCAAGCAGTTTGTGAAAAACCTGC	2851
QY	814		AsnThrGlnValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeu	833
Db	2852		AAACACTCAAGTCCACCTTTCATCCGAAGAGGCTGAATCATAAATATAACCCAGTGTCACTT	2911
QY	834		ProLysAspLeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGlu	853
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QY	854		LeuPheAlaValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLys	873
Db	2972		TTATTTGCTGTTCTCTGCATAGAAAACAAGCCACTATGTTGCTTTTGTGGAAGTATGGGAG	3031
QY	874		AspAspSerAlaTrpLeuPhePheAspSerMetAlaAspArgAspGlyGlyGlnAsnGly	893
Db	3032		GACGATTTGCTGCTGCTCTTTTGTGACGATGCCGATCGGATGGTGGTCAAGATGGC	3091
QY	894		PheAsnIleProGlnValThrProCysProGluValGlyGluTyrLeuLysMetSerLeu	913
Db	3092		TTCAACATTTCTCAAGTCACTCCCATGCCAAGAGTAGAGAGTACTTGAAGATGTCTCTG	3151
QY	914		GluAspLeuHisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCys	933
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RESULT 8
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LOCUS      Sequence 97 from Patent WO2004058805.
DEFINITION      CQ834226
ACCESSION      CQ834226
VERSION      CQ834226.1 GI:50833763
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE      1
AUTHORS      Matsuda,A. and Yoneta,S.
TITLE      T cell activating gene
JOURNAL      Patent: WO 2004058805-A 97 15-JUL-2004;
            Asahi Kasei Pharma Corporation (JP)
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            IFFGVELLEGGRCQGTDFGVQKQFQCDQEDCGFVALDKLELIEDDDTALRESVYG
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ORIGIN

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US-09-671-687A-3 (1-949) x CQ834226 (1-3311)

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      303  TTTTACTTGTCTTTCAGGAATGAGCGGTTCACAGACAAACAAACACAAAAGCTCCTTAAA 362

QY      41  ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle 60
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      363  GTACCGAAGGAAGTATAGGACAGTATATCAAGATCGTTCGTGGGGCATTTCAAGGATT 422

61  ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisIala 80
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      423  CCTTCTGCAAAAGGCAAGAAAAATCAGATTGGATTAATAAATTCCTAGAGCAACCTCATGCA 482

QY      81  ValLeuPheValAspGlu---AspValValGluIleAsnGluLysPheThrGluLeuLeu 99
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      483  GTTCTCTTGTGTGATGAAAAGGATGTTGTAGAGATAAATGAAAAAGTTTCACAGAGTTACTT 542

QY      100  LeuAlaIleThrAsnCysGluGluArgPheSerLeuPheLysAsnAtcAsnArgLeuSer 119
      |||
      543  TTGGCAATACCAATTTGTGAGGAGAGGTTTCAGCTGTTTAAAAAACAAGAAACAGACTAAGT 602

QY      120  LysGlyLeuGlnIleAspValGlyCysProValLysValGlnLeuArgSerGlyGluGlu 139
      |||
      603  AAGGCCCTCCAAATAGACGTGGGCTGCTCTGTGAAAGTACAGCTGAGATCTGGGGAAGNA 662

QY      140  LysPheProGlyValValAla:gpheArgGlyProLeuLeuAlaGluArgThrValSerGly 159
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      663  AAATTTCTCGAGTGTGACGCTTCAGAGGACCCCTGTAGCAGAGAGGACAGTCTCCGGA 722

QY      160  IlePhePheGlyValGluLeuLeuGluGluArgGlyGlnGlyPheThrAspGlyVal 179
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      723  ATATTCTTTGGAGTTGAATTGCTGGAAGAGGTCGTGTCGAAGGTTTCACGTACGGGGTG 782

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QY      199  LysLeuGluLeuIleGluAspAspThrAlaLeuGluLeuGluSerAspTyrAlaGlyProGly 218
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      843  AAGCTAGAACTCATAGAAGATGATGACATGTCATTGGAAAGTATTACGCAGGTCTCTGGG 902

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      |||
      903  GACAAATGCAAGGTGCGAACTTCCTCTTGGAAATAAACTCCAGAGTTTCTTTGAAGGT 962

QY      239  GlyGluThrIleGluSerGlyThrValIlePheCysAspValLeuProGlyLysGluSer 258
      |||
      963  GGAGAAACAATAGAAATCTGGAACAGTTATATTCTGTGATGTTTGGCCAGGAAAGAAAGC 1022

QY      259  LeuGlyTyrPheValGlyValAspMetAspAsnProIleGlyAsnTrpAspGlyArgPhe 278
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      1023  TTAGGATATTTTGTGTGTGGACATGATGATAACCTATTGGCAACTGGGATGGAAGATTT 1082

QY      279  AspGlyVal---LeuCysSerPheAlaCysValGluSerThrIleLeuLeuHisIleAsn 297
      |||
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QY      298  AspileIlePro-----GluSerValThrGlnGluArgAtgProProLysLeuAla 314
      |||
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QY      315  PheMetSerArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThr 334
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QY      354  SerSerValAspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluVal 373
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      1323  TCTTCTGTGTGACTCACAACCAATCCAAATCCAAATAATACAAAAATACATGTGTACATTGATGAAGTT 1382

QY      374  AlaGluAspProAlaLysSerLeuThrGluIleSerThrAspPheAspArgSerSerPro 393
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      1383  GCAGAAAGCCCTGCAAAATCTCTTACAGAGATATCTACAGACTTTGACCGTCTTCCACCA 1442

QY      394  ProLeuGlnProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuPro 413
      |||
      1443  CCACCTCCAGCCTCCTCTCTGTGAACCTCACTGACCCAGAGAAACAGATTCACCTCTTTACCA 1502

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Db 1563 TCAGCCCGAGTCTGTAATGGAAGAGCTAAACACTGCACCCGTCGAAGAGAGTCCACCCCTTG 1622  
Qy 454 AlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeuAlaGluValGlyGlu 473  
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Qy 494 LeuAlaGlyLeuGluLeuGluAspGluCysAlaGlyCysThrAspGlyThrPheArgGly 513  
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Qy 514 ThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArg 533  
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Qy 534 ProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIleGluArgCysAsnSer 553  
Db 1863 CTTGACTCTAGTTTGCATCATTCAGCCGGTTCCTAATCAGATTGAGCGCTGTAACCTCT 1922  
Qy 554 LeuAlaPheGlyGlyTyrLeuSerGluValValGluGluAsnThrProProLysMetGlu 573  
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Qy 754 LysAspPheLysLeuPheLysIlePheProSerLeuGluLeuAsnIleThrAspLeu 773  
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VERSION CQ719792.1 GI:42280649  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
TITLE Kits, such as nucleic acid arrays, comprising a majority of  
humanexons or transcripts, for detecting expression and other uses  
thereof  
JOURNAL Patent: WO 02068579-A 5726 06-SEP-2002;  
PE Corporation (NY) (US)  
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Best Local Similarity: 99.27% Mismatches: 2  
Query Match: 98.57% Indels: 5  
DB: 6 Gaps: 4

US-09-671-687A-3 (1-949) x CQ719792 (1-3480)

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Db	295	TTTTACTTGTCTTCTCAAGAAATCAGCGTTACAGACAAACAAACAAAAGCTCTTTAA	354	Db	1375	CCCTGCAAAATCTCTTACAGAGATATCTACAGACTTTGACCGTTCTTCCACCACCACTCCA	1434
Qy	41	ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgile	60	Qy	396	nProProProValAsnSerLeuThrThrGluAsnArgPheHisSerLeuProPheSerile	416
Db	355	GTACCGAAGGGAAGTATAGGACAGTATATCAAGATCGTTCTGTGGGCGATTCAAGGATT	414	Db	1435	GCCTCCTCTGTGAACCTCACTGACCACCGAGAACAGATTCCACTCTTTTACCATTTCAGTCT	1494
Qy	61	ProSerAlaLysGlyLysLysAsnGlnIleGlyLeuLysIleLeuGluGlnProHisAla	80	Qy	416	uThrLysMetProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGlu	436
Db	415	CCTTCTGCAAAAGGCAAGAAATAATCAGATTGGATTAAATAATTCAGAGCAACCTCATGCA	474	Db	1495	CACCAAGATGCCCAATACCAATGGAAGTATTGGCCACAGTCCACTTTCTGTGACGCCA	1554
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Db	475	GTCTCTTTGTGTGATAAAGGATGTTGTAGAGATAAATGAAAGTTTCAACAGATTACTT	534	Db	1555	GTCTGTAATGGAAAGCTAAACACTGCACCCGTCACAGAGAGTCCACCCTTGGCCATGCC	1614
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Db	655	AAATTTCTGGAGTTGTACGCTTCAGAGGACCCCTGTTTAGCAGAGAGACAGTCTCCGGA	714	Db	1735	ACTGGAACTGGAAAGATGAGTGTGAGGCTGTACGGATGGAACCTTCAGAGGCACCTCGGTA	1794
Qy	160	IlePhePheGlyValGluLeuLeuGluGluGlyArgGlyGlnGlyPheThrAspGlyVal	179	Qy	516	rPheThrCysAlaLeuLysLysAlaLeuPheValLysLeuLysSerCysArgProAspSe	536
Db	715	ATATTTCTGGAGTTGAATTCGTGGAAGAGTCTGTGTCGAAGGTTTCACTGACGGGGTG	774	Db	1795	TTTCACCTGTGCCCTGGAAGAGGCGCTGTTTGTGAAACTGAAGAGCTGCAGGCCCTGACTC	1854
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Qy	219	AspThrMetGlnValGluLeuProProLeuGluIleAsnSerArgValSerLeuLysGly	238	Qy	576	yLeuGluIleMetIleGlyLysLysLysGlyIleGlnGlyHisTyrAsnSerCysTyrIle	596
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Db	1135	GATATCATCCAGAGAGTGTACGACGAGAAGAGGCGCTCCCAAACTTCCTTTATGTCA	1194	Db	2215	GAAATACTTGAAAGGTGGAGGCTGCATCAGGATTTTACCTCTGAAGAAAAAGATCCTGA	2274
Qy	318	ArgGlyValGlyAspLysGlySerSerHisAsnLysProLysAlaThrGlySerThr	337	Qy	676	uGluPheLeuAsnIleLeuPheHisIleLeuArgValGluProLeuLeuLysIleAr	696
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ACCESSION BD231207  
VERSION 1  
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SOURCE Homo sapiens (human)  
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REFERENCE  
AUTHORS Lal,P., Tang,T.Y., Yue,H., Hillman,J.L., Bandman,O., Corley,N.C.,  
Guegler,K.O., Patterson,C., Azimzai,Y. and Baughn,M.R.  
TITLE Human cytoskeleton associated proteins  
JOURNAL Patent: JP 2002526076-A 9 20-AUG-2002;  
INCYTE PHARMACEUTICALS INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002526076-A/9  
PD 20-AUG-2002  
PF 17-SEP-1999 JP 2000574254  
PR 18-SEP-1998 US 60/172226,27-APR-1999 US 60/131321 PI  
PREETI LAL,TOM Y TANG,HENRY YUE,JENNIFER L HILLMAN,OLGA PI  
BANDMAN,  
PI NEIL C CORLEY,KARL J GUEGLER,CHANDRA PATTERSON,YALDA AZIMZAI,  
PI MARIAH R BAUGHN  
PC C12N15/09,A61K38/00,A61K45/00,A61P1/16,A61P3/00,A61P3/06 PC  
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Qy	420	ProAsnThrAsnGlySerIleGlyHisSerProLeuSerLeuSerAlaGlnSerValMet	439
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Qy	720	ValProThrIleGlnGlnLeuLeuGluTrpSerPheIleAsnSerAsnLeuLysPheAla	739
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Qy	740	GluAlaProSerCysLeuIleIleGlnMetProArgPheGlyLysAspPheLysLeuPhe	759
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LOCUS Mus musculus mRNA for mKIAA0849 protein.
DEFINITION AKI22389
ACCESSION VERSION
KEYWORDS FLI CDNA.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Okazaki,N., Kikuno,R., Ohara,R., Inamoto,S., Aizawa,H., Yuasa,S.,
Nakajima,D., Nagase,T., Ohara,O. and Koga,H.
TITLE Prediction of the coding sequences of mouse homologues of KIAA
gene: II. The complete nucleotide sequences of 400 mouse
KIAA-homologous cDNAs identified by screening of terminal sequences
of cDNA clones randomly sampled from size-fractionated libraries
JOURNAL DNA Res. 10, 35-48 (2003)
AUTHORS Okazaki,N., Kikuno,R., Ohara,R., Inamoto,S., Aizawa,H., Yuasa,S.,
Nakajima,D., Nagase,T., Ohara,O. and Koga,H.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-2003) Hisashi Koga, Kazusa DNA Research
Institute, Laboratory for Genome Informatics; 2-6-7
Kazusa-Kamatar, Kisarazu, Chiba 292-0818, Japan
(E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)
COMMENT The CREATE program supported by Japan science and technology
corporation; cDNA full insert sequencing; Kazusa DNA Research
Institute; cDNA library construction, clone selection and 5'- &
3'-end one pass sequencing.
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location/Qualifiers
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## ORIGIN

## Alignment Scores:

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Pred. No.: 0 Length: 4314
Score: 4718.50 Matches: 898
Percent Similarity: 96.54% Conservative: 22
Best Local Similarity: 94.23% Mismatches: 28
Query Match: 93.73% Indels: 5
DB: 9 Gaps: 5

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US-09-671-687A-3 (1-949) x AKI22389 (1-4314)

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Db 398 TTTTATCTGCTTCTTCAAGAAATGCAGTGTAAACAGACAAACAACTCAGAAGCTGCTGAAA 457
Qy 41 ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisArgIle 60
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ACCESSION BC042438
VERSION BC042438.1 GI:27503670
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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 4501)
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AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zebberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettaman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Greenchenko, Y., Boufaraz, G.G., Blakesley, R.W., Touchman, J.W., Sheen, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932

2 (bases 1 to 4501)

Strausberg, R.

Direct Submission

Submitted (02-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegod, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

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ORIGIN

Alignment Scores:

Pred. No.: 0 Length: 4501  
Score: 4718.50 Matches: 898  
Percent Similarity: 96.54% Conservative: 22  
Best Local Similarity: 94.23% Mismatches: 28  
Query Match: 93.73% Indels: 5  
DB: 9 Gaps: 5

US-09-671-687A-3 (1-949) x BC042438 (1-4501)

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FEATURES

source

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAX Plate: 30 Row: 9 Column: 3.

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BC082001  
LOCUS  
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(predicted), mRNA (cdna clone MGC:94236 IMAGE:7131198), complete  
cds

ACCESSION

BC082001 GI:51858716

VERSION

BC082001.1

KEYWORDS

MGC.

SOURCE

Rattus norvegicus (Norway rat)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Rattus.

REFERENCE

1 (bases 1 to 3267)

AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Sheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullany, S.J., Bosak, S.A., McSwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,  
Sanchez, A., Whiting, M., Madan, M., Young, A.C., Shevchenko, Y.,  
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

CONSTRM

TITLE

Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences

JOURNAL

PUBLISHED

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

REFERENCE

2 (bases 1 to 3267)

AUTHORS

CONSTRM

TITLE

NIH MGC Project  
Direct Submission  
Submitted (01-SEP-2004) National Institutes of Health, Mammalian  
Gene Collection (MGC), Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)  
Tissue Procurement: Howard Jacobs  
cdna Library Preparation: Express Genomics  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.

REMARK

COMMENT

Clone distribution: MGC clone distribution information can be found  
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Series: IRAK Plate: 184 Row: j Column: 24  
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FEATURES

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ORIGIN

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Query Match: 93.60% Indels: 4  
DB: 9 Gaps: 4

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DB 2236 GAATTTCTAAACATCCTCTTTCATGATATTTTAAAGGGTTGAACCATTTGTTAAAAATPAAG 2295  
QY 697 SerAlaGlyGlnLysValGlnAspCysTyrPheTyrGlnIlePheMetGluLysAsnGlu 716  
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DB 2416 AAATTTGCAGAGGCCACCATCATGCTTGATTAATCCAGATGCCCTCGGTTTGGGAAAGACTTT 2475  
QY 757 LysLeuPheLysIlePheProSerLeuGluLeuAsnIleThrAspLeuLeuGluAsp 776  
DB 2476 AAATTTTAAAAAATTTTTTCTTCCCTGGAAATTTAAATATAACAGATTTACTTTGAAGAC 2535  
QY 777 ThrProArgGlnCysArgIleCysGlyGlyLeuAlaMetTyrGluCysArgGluCysTyr 796  
DB 2536 ACTCCCGCAGTGGCGCATCTGTGAGGAGCTCGCCATGATGATGATGATGATGATGATGAT 2595  
QY 797 AspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrGln 816  
DB 2596 GATGACCCGGACATCTCGCAGGGAAGATCAAGCAGTTCTGTAAAGACCTTCGACACTCAG 2655  
QY 817 ValHisLeuHisProLysArgLeuAsnHisLysTyrAsnProValSerLeuProLysAsp 836  
DB 2656 GTTACCTTCATCCCAAGAGACTGAAATCACATTTACCATCCAGTATCACTTCCCAAGAC 2715  
QY 837 LeuProAspTrpAspTrpArgHisGlyCysIleProCysGlnAsnMetGluLeuPheAla 856  
DB 2716 TTGCCCGACTGGGACTGGAGACACGCTGCATCCCGTGTGAGAAAGATGGAGTTATTGCT 2775  
QY 857 ValLeuCysIleGluThrSerHisTyrValAlaPheValLysTyrGlyLysAspAspSer 876  
DB 2776 GTGCTCTGCATAGAAACACAGCCACTATGTTGCTTTTGTGAAGTACGGGAGGATGACTCT 2835  
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Qy      917 HisSerLeuAspSerArgArgIleGlnGlyCysAlaArgArgLeuLeuCysAspAlaTyr 936
Db      2956 CACTCTTTGGACTCCAGAGGATTCAAGGCTGTGCGGCAGACTTCTTGGATGCATAC 3015
Qy      937 MetCysMetTyrGlnSerProThrMetSerLeuTyrLys 949
Db      3016 ATGTGATGTACAGAGTCAACCATGAGCTTGACAAA 3054

RESULT 14
BD160617 2845 bp DNA linear PAT 17-JAN-2003
LOCUS Primer for synthesizing full-length cDNA and use thereof.
DEFINITION BD160617
ACCESSION BD160617
VERSION BD160617.1 GI:27866375
KEYWORDS JP 2002191363-A/15460.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 2845)
Ota.T., Isogai.T., Nishikawa.T., Hayaashi.K., Saito.K., Yamamoto.J.,
Ishii.S., Sugiyama.T., Wakamatsu.A., Nagai.K. and Otsuki.T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 15460 09-JUL-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002191363-A/15460
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUUI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10,
PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof PH Key
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(452)..(2644).
LOCATION/Qualifiers
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Alignment Scores:
Pred. No.: 0 Length: 2845
Score: 4601.00 Matches: 875
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DB: 6 Gaps: 4

US-09-671-687A-3 (1-949) x BD160617 (1-2845)

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Qy 92 AsnGluLysPheThrGluLeuLeuAlaIleThrAsnGluGluArgPheSerLeu 111
Db 62 AATGAAAGTTTACAGAGTTACTTTTGGCAATTAACCAATTTGTCAGGAGAGTTTCAGCCTG 121
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Qy 132 ValGlnLeuArgSerGlyGluLysPheProGlyValValatqPheArgGlyProLeu 151
Db 182 GTACAGCTGAGATCTGGGGAAGAAAATTTCTTGAGTTGTACGCTTTCAGAGACCCCTG 241
Qy 152 LeuAlaGluArgThrValSerGlyIlePhePheGlyValGluLeuLeuGluGlyArg 171
Db 242 TTACACAGAGGACAGCTCTCGGAATATTTCTTGAGTTGAATTCGTGGAAGAAGTCTGT 301
Qy 172 GlyGlnGlyPheThrAspGlyValTyrGlnGlyLysGlnLeuPheGlnCysAspGluAsp 191
Db 302 GGTCAAGGTTTCACTGACGGGGTGTACCAAGGGAACACAGCTTTTTCAGTGTGATGAAGAT 361
Qy 192 CysGly---PheValAlaLeuAspLysLeuLeuIleGluAspAspAspThrAlaLeu 210
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Qy 211 GluSerAspTyrAlaGlyProGlyAspThrMetGlnValGluLeuProProLeuGluIle 230
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Db 722 CCTCCCAAATCTGCTTTATGTCAAGAGGTGTTGGGGACAAAGGTTCTATCCAGTCATAT 781
Qy 330 LysProLysAlaThrGlySerThrSerAspProGlyAsnArg---ArgSerGluLeuPhe 348
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Qy 429 SerProLeuSerLeuSerAlaGlnSerValMetGluLeuLeuAsnThrAlaProValGln 448
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Qy 449 GluSerProProLeuAlaMetProProGlyAsnSerHisGlyLeuGluValGlySerLeu 468
Db 1142 GAGAGTCCACCCCTGGCCATGCTCTCTGGGAATCTACATGGTCTAGAAAGTGGGCTCAT 1201
Qy 469 AlaGluValLysGluAsnProPheTyrGlyValIleArgTrpIleGlyGlnProPro 488
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Qy      489  GlyLeuAsnGluValLeuAlaGlyLeuGluLeuGluAspGluCysAlaGlyCysThrAsp 508
Db      1262  GGAAGTGAATGAAGTGCCTGCTGGACCTGGAATCGAAGATGATGTCAGGCTGTACCGAT 1321
Qy      509  GlyThrPheArgGlyThrArgTyrPheThrCysAlaLeuLysLysAlaLeuPheValLys 528
Db      1322  GGAACCTTCAGAGGCACTCGGTATTTTACCTGTGCTCCCTGGAAGAGGCGCTGTTGTGAA 1381
Qy      529  LeuLysSerCysArgProAspSerArgPheAlaSerLeuGlnProValSerAsnGlnIle 548
Db      1382  CTGAAGAGCTGCAGGCTGACTCTAGGTTTGCATCATTTGCAGCGGTTTCCAAATCAGATT 1441
Qy      549  GluArgCysAsnSerLeuAlaPheGlyClyTyrLeuSerGluValValGluGluAsnThr 568
Db      1442  GAGCGCTGTAACCTCTTTAGCATTTTGGAGGCTACTTAAGTAGTAAGTAAAGAAATACT 1501
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Qy      689  ValGluProLeuLeuLysIleArgSerAlaGlyGlnLysValGlnAspCysTyrPheTyr 708
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Qy      709  GlnIlePheMetGluLysAsnGluLysValGlyValProThrIleGlnGlnLeuLeuGlu 728
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Db      1982  TGGTCTTTTATCAACAGTAACCTGAAATTTTCAGAGGCGACCATCATGCTCATATTTCAG 2041
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Db      2042  ATGCTCTGATTGGAAAAAGACTTTAAACTATTTAAAAAATTTTTCCTCTCTCTGGAATTA 2101
Qy      769  AsnIleThrAspLeuLeuGluAspThrProArgGlnCysArgIleCysGlyGlyLeuAla 788
Db      2102  AATATAACAGATTTACTTTGAAGACACTCCCAAGACGTCCCGGATGTGGAGGGCTTGCA 2161
Qy      789  MetTyrGluCysArgGluCysTyrAspAspProAspIleSerAlaGlyLysIleLysGln 808
Db      2162  ATGTATGAGTGTAGAGATGCTACGACGATCCGACATCTCAGCTGGAAAAATCAAGCAG 2221
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Qy      869  ValLysTyrGlyLysAspAspSerAlaTyrLeuPhePheAspSerMetAlaAspArgAsp 888
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Qy      889  GlyGlyGlnAsnGlyPheAsnIleProGlnValThrProCysProGluValGlyGluTyr 908
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Qy      909  LeuLysMetSerLeuGluAspLeuHisSerLeuAspSerArgArgIleGlnGlyCysAla 928
Db      2522  TTGAAGATGCTCTGGAAGACCTGCATTTCTTGGACTCCAGGAGAAATCAAGGCTGTGCA 2581
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RESULT 15
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LOCUS Sequence 18842 from Patent EP1074617.
ACCESSION AX883937
VERSION AX883937.1 GI:40039838
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
REFERENCE
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primers for synthesising full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 18842 07-FEB-2001;
RESEARCH Association for Biotechnology (JP)
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Alignment Scores:
Pred. No.: 0 Length: 2845
Score: 4601.00 Matches: 875
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US-09-671-687A-3 (1-949) x AX883937 (1-2845)

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QY 549 GluArgCysAsnSerLeuAlaPheGlyGlyTyrLeuSerGluValValGluGluAsnThr 568
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QY 589 GlyHisTyrAsnSerCysTyrLeuAspSerThrLeuPheCysLeuPheAlaPheSerSer 608
DB 1562 GGTCAATTCACATCTCTGTTACTTAGACTCAACCTTATCTGCTTATTTGCTTTAGTTCT 1621
QY 609 ValLeuAspThrValLeuLeuArgProLysGluLysAsnAspValGluTyrTyrSerGlu 628
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 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R.,  
 Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,  
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 Complete sequencing and characterization of 21,243 full-length  
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 Nat. Genet. 36 (1), 40-45 (2004)  
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 JOURNAL  
 PUBMED  
 REFERENCE  
 AUTHORS  
 Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,  
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 NEDO human cDNA sequencing project  
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 3 (bases 1 to 2845)  
 Isogai,T. and Otsuki,T.  
 Direct Submission  
 Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,  
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 (E-mail: genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
 NEDO human cDNA sequencing project supported by Ministry of  
 International Trade and Industry of Japan; cDNA full insert  
 sequencing: Research Association for Biotechnology; cDNA library  
 construction, 5'- & 3'-end one pass sequencing and clone selection:  
 Helix Research Institute (supported by Japan Key Technology Center  
 etc.) and Department of Virology, Institute of Medical Science,  
 University of Tokyo.  
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 QY 92 AsnGluLysPheThrGluLeuLeuAlaIleThrAsnCysGluGluArgPheSerLeu 111  
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 Db 122 TTTTAAAAACAGAAACACAGACTAAGTAAAGGCCCTCCAAATAGACGTGGGCTGCTCTGTGAAA 181  
 QY 132 ValGlnLeuArgSerGlyGluGluLysPheProGlyValValArgPheArgGlyProLeu 151  
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AC123449			
LOCUS			
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ACCESSION	AC123449		
VERSION	AC123449.3	GI:23265406	
KEYWORDS	HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
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US-09-671-687A-3 (1-949) x AC123449 (1-241990)

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DB 206331 AGAGGTGTAGTGACAAAGGCTCATCTAGTATAATAAACCAAGGTTTACAGGATCTACC 206390  
QY 338 SerAspProGlyAsnArg---ArgSerGluLeuPheTyrThrLeuAsnGlySerSerVal 356  
DB 206391 TCAGACCTCGAAGTAGAAACAGATCTGAATTTATTTATACCTTAAATGGGTTCATCTGT 206450  
QY 357 AspSerGlnProGlnSerLysSerLysAsnThrTrpTyrIleAspGluValAlaGluAsp 376  
DB 206451 GACTCAACAACAATCCAGTCCAAAACCCATGGTACATTGATGAAGTTGCAGAGAC 206510  
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Db 207651 TTAACATATTAAAAAATTTTCTCTCCCTGGGAATTAATATGACAGATTTACTTGAAG 207710  
  
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Db 207711 ACATCTCCAGCGAGTCGCCGATCTGTGCGAGGACTCGCCATGTATGAGGTAGAGAGTGCT 207770  
  
796 yrAspAspProAspIleSerAlaGlyLysIleLysGlnPheCysLysThrCysAsnThrG 816  
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RESULT 18

AC098162/c

LOCUS

DEFINITION Rattus norvegicus clone CH230-3014, \*\*\* SEQUENCING IN PROGRESS \*\*\*,

3 unordered pieces.

## ACCESSION

AC098162.7 GI:30522215

VERSION HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_ENRICHED.

KEYWORDS Rattus norvegicus (Norway rat)

## SOURCE

ORGANISM  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eultheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Murioidea; Muridae; Murinae; Rattus.

1 (bases 1 to 251132)

## REFERENCE

## AUTHORS

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Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,  
Weinstock, G. and Gibbs, R. A.

Direct Submission

Unpublished

2 (bases 1 to 251132)

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

Submitted (23-OCT-2001)

Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 251132)

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

Submitted (10-MAY-2003)

Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:24819609.

The sequence in this assembly is a combination of BAC based reads and whole genome sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information

Center project name: GGWL

Center clone name: CH230-3014

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 241087 bases at least Q40

Consensus quality: 243305 bases at least Q30

Consensus quality: 244914 bases at least Q20

Estimated insert size: 256850; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

-----

\* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html))  
 \* NOTE: This sequence may represent more than one clone.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 3 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 248387: contig of 248387 bp in length  
 \* 248388 248487: gap of unknown length  
 \* 248488 249536: contig of 1049 bp in length  
 \* 249537 249637: gap of unknown length  
 \* 249637 251132: contig of 1496 bp in length.

#### FEATURES

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 /clone="CH230-3014"

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##### misc\_feature

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 /note="clone boundary  
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 site:EcoRI

##### misc\_feature

end sequence:BH292593"  
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 /estimated\_length=unknown  
 249537..249636  
 /estimated\_length=unknown

##### gap

248388..249487

##### gap

249537..249636

#### ORIGIN

##### Alignment Scores:

Pred. No.: 0 Length: 251132  
 Score: 4600.50 Matches: 883  
 Percent Similarity: 95.29% Conservative: 27  
 Best Local Similarity: 92.46% Mismatches: 38  
 Query Match: 91.39% Indels: 8

DB:	14	Gaps:	5
US-09-671-687A-3 (1-949) x AC098162 (1-251132)			
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Qy	41	ValProLysGlySerIleGlyGlnTyrIleGlnAspArgSerValGlyHisSerArgIle	60
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[illegible]